

GenCore version 5.1.6
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nucleic - nucleic search, using sw model

on: November 8, 2003, 01:25:59 ; Search time 244 Seconds

(without alignments)
274.632 Million cell updates/sec

let: US-09-944-326-4

fect score: 21

fluence: 1

ring table: IDENTITY NUC

atched: 214354 seqs, 1595478879 residues

imum DB seq length: 0

imum DB seq length: 2000000000

ic-processing: Minimum Match 0%

Listing first 45 summaries

abase : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	12	US-09-967-726A-4
3	21	100.0	21	12	US-10-080-794-4
4	21	100.0	396	9	US-09-825-284-15
5	21	100.0	396	10	US-09-870-866-15
6	21	100.0	396	15	US-10-212-677-15
7	21	100.0	461	11	US-09-918-995-32172
8	21	100.0	462	11	US-09-918-995-2524
9	21	100.0	465	11	US-09-918-995-32177
10	21	100.0	490	11	US-09-918-995-12511
11	21	100.0	491	11	US-09-918-995-17455
12	21	100.0	492	11	US-09-918-995-31156
13	21	100.0	532	10	US-09-833-381-910
14	21	100.0	1451	12	US-10-133-013-214
15	21	100.0	1614	12	US-10-119-428-31
16	21	100.0	1678	10	US-09-765-231A-16

C 17	21	100.0	1775	12	US-10-133-013-243	Sequence 243, App
C 18	20	95.2	277	10	US-09-833-381-1241	Sequence 1241, Ap
C 19	19.4	92.4	123	10	US-09-783-590-3282	Sequence 3282, Ap
C 20	19.4	92.4	539	11	US-09-918-995-31688	Sequence 31688, A
C 21	17.8	84.8	21	12	US-09-967-726A-15	Sequence 15, App1
C 22	17.8	84.8	21	12	US-10-080-794-15	Sequence 15, App1
C 23	17.8	84.8	366	10	US-09-960-352-188	Sequence 188, App
C 24	17.8	84.8	377	10	US-09-960-352-3858	Sequence 3858, App
C 25	17.8	84.8	379	10	US-09-960-352-6621	Sequence 6621, Ap
C 26	17.8	84.8	389	10	US-09-960-352-14093	Sequence 14093, A
C 27	17.8	84.8	413	10	US-09-960-352-2490	Sequence 2490, Ap
C 28	17.8	84.8	414	10	US-09-960-352-2489	Sequence 2489, Ap
C 29	17.8	84.8	414	10	US-09-960-352-10772	Sequence 10772, A
C 30	17.8	84.8	416	10	US-09-960-352-8509	Sequence 8509, Ap
C 31	17.8	84.8	426	10	US-09-960-352-6031	Sequence 6031, Ap
C 32	17.8	84.8	462	12	US-10-027-632-292190	Sequence 292190, Ap
C 33	17.8	84.8	462	13	US-10-027-632-292190	Sequence 292190, Ap
C 34	17.8	84.8	2239	12	US-10-027-632-111116	Sequence 111116, Ap
C 35	17.8	84.8	2239	12	US-10-027-632-111117	Sequence 111117, Ap
C 36	17.8	84.8	2239	13	US-10-027-632-111116	Sequence 111116, Ap
C 37	17.8	84.8	2239	13	US-10-027-632-111117	Sequence 111117, Ap
C 38	17.4	82.9	300	10	US-09-941-997-1	Sequence 1, App1
C 39	17.4	82.9	379	11	US-09-918-995-3993	Sequence 3993, Ap
C 40	17.4	82.9	396	11	US-09-918-995-3872	Sequence 3872, Ap
C 41	17.4	82.9	407	11	US-09-918-995-2976	Sequence 2976, Ap
C 42	17.4	82.9	415	11	US-09-918-995-5801	Sequence 5801, Ap
C 43	17.4	82.9	441	11	US-09-918-995-3798	Sequence 3798, Ap
C 44	17.4	82.9	455	11	US-09-918-995-5994	Sequence 5994, Ap
C 45	17.4	82.9	481	11	US-09-918-995-4221	Sequence 4221, Ap

ALIGNMENTS

RESULT 1
US-09-944-326-4
Sequence 4, Application US/09944326
Patent No. US20020128220A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
FILE REFERENCE: UBC-P-020-2
CURRENT APPLICATION NUMBER: US/09/944,326
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 21
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4

Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGCTCTCATCAT 21
Db 1 CAGCAGCAGCTCTCATCAT 21

RESULT 2
US-09-967-726A-4
Sequence 4, Application US/09967726A

Application No. US20030158130A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
APPLICANT: Zellweger, Tobias
TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
FILE REFERENCE: USC-P-022
CURRENT APPLICATION NUMBER: US/09/967,726A
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 4
LENGTH: 21
TYPE: DNA
ORGANISM: human
9-967-726A-4

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
1 CAGCAGCAGAGCTTTCATCAT 21

LT 3
0-080-794-4
Sequence 4, Application US/10080794
Application No. US20030156591A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
APPLICANT: Monla, Brett P.
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
FILE REFERENCE: USC-P-020-3
CURRENT APPLICATION NUMBER: US/10/080,794
CURRENT FILING DATE: 2002-02-22
RIOR APPLICATION NUMBER: 60/121,726
RIOR FILING DATE: 1999-02-26
RIOR APPLICATION NUMBER: 09/913,325
RIOR FILING DATE: 2001-08-10
RIOR APPLICATION NUMBER: 09/944,326
RIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 21
TYPE: DNA
ORGANISM: HUMAN
FEATURES:
OTHER INFORMATION: antisense TRPM-2 ODN
0-080-794-4

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
1 CAGCAGCAGAGCTTTCATCAT 21

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-15

Query Match 100.0%; Score 21; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
79 CAGCAGCAGAGCTTTCATCAT 59

RESULT 5
US-09-970-966-15/c
Sequence 15, Application US/09970966
Patent No. US20020173638A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Molesch, David Alan
APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: 333
OTHER INFORMATION: n = A,T,C or G
US-09-970-966-15

Query Match 100.0%; Score 21; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
79 CAGCAGCAGAGCTTTCATCAT 59

RESULT 6
US-10-212-677-15/c
Sequence 15, Application US/10212677
Publication No. US20030129192A1
GENERAL INFORMATION:
APPLICANT: Chennault, Ruth A.
APPLICANT: Xu, Jiangchun

APPLICANT: Fanger, Gary R.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: McNeill, Patricia D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 210121.484C7
 CURRENT APPLICATION NUMBER: US/10/212,677
 CURRENT FILING DATE: 2002-08-02
 NUMBER OF SEQ ID NOS: 288
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 15
 LENGTH: 396
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 333
 OTHER INFORMATION: n = A,T,C or G
 -10-212-677-15

Query Match 100.0%; Score 21; DB 15; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 79 CAGCAGCAGAGCTTCATCAT 59

SULT 7
 -09-918-995-32172/c
 Sequence 32172, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 32172
 LENGTH: 461
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) --(461)
 OTHER INFORMATION: n = A,T,C or G
 -09-918-995-32172

Query Match 100.0%; Score 21; DB 11; Length 461;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 130 CAGCAGCAGAGCTTCATCAT 110

TUT 8
 -09-918-995-2524/c
 Sequence 2524, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2524
 LENGTH: 462
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) --(462)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-2524

Query Match 100.0%; Score 21; DB 11; Length 462;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
 Db 115 CAGCAGCAGAGCTTCATCAT 95

RESULT 9
 US-09-918-995-32177/c
 Sequence 32177, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 32177
 LENGTH: 465
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) --(465)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-32177

Query Match 100.0%; Score 21; DB 11; Length 465;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
 Db 122 CAGCAGCAGAGCTTCATCAT 102

RESULT 10
 US-09-918-995-12511/c
 Sequence 12511, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0

EQ ID NO 12511
 LENGTH: 490
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(490)
 OTHER INFORMATION: n = A,T,C or G
 09-918-995-12511

Query Match 100.0%; Score 21; DB 11; Length 490;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 123 CAGCAGCAGAGCTTCATCAT 103

JLT 11
 09-918-995-17455/C
 Sequence 17455, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918, 995
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 17455
 LENGTH: 491
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(491)
 OTHER INFORMATION: n = A,T,C or G
 09-918-995-17455

Query Match 100.0%; Score 21; DB 11; Length 491;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 134 CAGCAGCAGAGCTTCATCAT 114

JLT 12
 09-918-995-31156/C
 Sequence 31156, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918, 995
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 31156
 LENGTH: 492
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:

NAME/KEY: misc.feature
 LOCATION: (1)...(492)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-31156

Query Match 100.0%; Score 21; DB 11; Length 492;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGCTTCATCAT 21
 Db 108 CAGCAGCAGAGCTTCATCAT 88

RESULT 13
 US-09-833-381-910/C
 Sequence 910, Application US/09833381
 Patent No. US20020132090A1
 GENERAL INFORMATION:
 APPLICANT: Robison, Keith E.
 TITLE OF INVENTION: NO. US20020132090A1 Nucleic Acid and Protein Homologs
 FILE REFERENCE: 5800-119
 CURRENT APPLICATION NUMBER: US/09/833,381
 PRIOR FILING DATE: 2001-04-11
 PRIOR APPLICATION NUMBER: 09/516,448
 NUMBER OF SEQ ID NOS: 2050
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 910
 LENGTH: 532
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(532)
 OTHER INFORMATION: n = A,T,C or G
 US-09-833-381-910

Query Match 100.0%; Score 21; DB 10; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGCTTCATCAT 21
 Db 93 CAGCAGCAGAGCTTCATCAT 73

RESULT 14
 US-10-133-013-214/C
 Sequence 214, Application US/10133013
 Publication No. US20030166903A1
 GENERAL INFORMATION:
 APPLICANT: Astromoff, Anna
 APPLICANT: Bandman, Olga
 APPLICANT: Cocke, Benjamin G.
 TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
 FILE REFERENCE: PA-0049 US
 CURRENT APPLICATION NUMBER: US/10/133,013
 PRIOR FILING DATE: 2002-04-25
 PRIOR APPLICATION NUMBER: 60/287,067
 NUMBER OF SEQ ID NOS: 271
 SOFTWARE: PERL Program
 SEQ ID NO 214
 LENGTH: 1451
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 OTHER INFORMATION: Incyte ID No. US20030166903A1 474437.17
 NAME/KEY: unsure
 LOCATION: 1407

OTHER INFORMATION: a, t, c, g, or other
-10-133-013-214

Query Match 100.0%; Score 21; DB 12; Length 1451;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
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366 CAGCAGCAGAGTCTTCATCAT 346

3ULT 15
-10-119-428-31/c
Sequence 31, Application US/10119428
Publication No. US20030165861A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Wehrman, Tom
APPLICANT: Ren, Feiyan
APPLICANT: Ma, Yungqing
APPLICANT: Zhou, Ping
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonhong
APPLICANT: Drmanac, Radcoje T.
TITLE OF INVENTION: No. US20030165861A1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,428
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: pc_FL_genes Version 1.0
SEQ ID NO 31
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (116)..(1465)
10-119-428-31

Query Match 100.0%; Score 21; DB 12; Length 1614;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAGCAGCAGAGTCTTCATCAT 21
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136 CAGCAGCAGAGTCTTCATCAT 116

rch completed: November 8, 2003, 02:48:52
time : 245 secs

GenCore version 5.1.6
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nucleic - nucleic search, using sw model

on: November 8, 2003, 00:46:13 ; Search time 70 Seconds
(without alignments)
132.415 Million cell updates/sec

le: US-09-944-326-4

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Gapop 10.0, Gapext 1.0

arched: 569978 segs, 220691566 residues

al number of hits satisfying chosen parameters: 1139956

imum DB seq length: 0
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it-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	21	100.0	181	2	US-08-485-657A-19 Sequence 19, Appl
2	21	100.0	181	4	US-09-366-380-19 Sequence 19, Appl
3	21	100.0	181	5	PCT-US95-02303-18 Sequence 18, Appl
4	21	100.0	195	2	US-08-485-657A-14 Sequence 14, Appl
5	21	100.0	195	4	US-09-366-380-14 Sequence 14, Appl
6	21	100.0	195	5	PCT-US95-02303-14 Sequence 14, Appl
7	21	100.0	1648	4	US-09-659-791A-3 Sequence 3, Appl
8	21	100.0	1651	4	US-09-659-791A-13 Sequence 13, Appl
9	21	100.0	7610	4	US-09-659-791A-12 Sequence 12, Appl
10	17.4	82.9	633	3	US-08-950-925-1 Sequence 1, Appl
11	17.4	82.9	633	4	US-09-565-286-1 Sequence 1, Appl
12	17.4	82.9	651	2	US-08-961-858-1 Sequence 1, Appl
13	17.4	82.9	651	2	US-08-961-858-1 Sequence 1, Appl
14	17.4	82.9	651	3	US-09-089-593-1 Sequence 3, Appl
15	17.4	82.9	651	3	US-09-089-593-1 Sequence 3, Appl
16	17.4	82.9	651	3	US-09-089-593-3 Sequence 3, Appl
17	17.4	82.9	744	4	US-09-368-819A-1 Sequence 1, Appl
18	17.4	82.9	795	4	US-09-368-819A-1 Sequence 1, Appl
19	17.4	82.9	1173	3	US-08-993-380-3 Sequence 3, Appl
20	16.8	80.0	330	2	US-08-980-060-9 Sequence 9, Appl
21	16.8	80.0	330	3	US-09-307-185-9 Sequence 9, Appl
22	16.8	80.0	334	4	US-09-227-357-90 Sequence 90, Appl
23	16.8	80.0	1806	3	US-09-307-185-1 Sequence 1, Appl
24	16.8	80.0	1806	3	US-09-307-185-1 Sequence 1, Appl
25	16.8	80.0	3459	2	US-08-980-060-3 Sequence 3, Appl
26	16.8	80.0	3459	2	US-09-307-185-3 Sequence 3, Appl
27	16.4	78.1	1051	3	US-09-008-697A-21 Sequence 21, Appl

28	16.2	77.1	32	4	US-09-410-935B-6 Sequence 6, Appl1
29	16.2	77.1	139	4	US-09-345-882-12 Sequence 12, Appl
30	16.2	77.1	279	4	US-09-313-294A-2815 Sequence 2815, Ap
31	16.2	77.1	283	4	US-09-313-294A-1242 Sequence 1242, Ap
32	16.2	77.1	336	4	US-09-657-452A-17 Sequence 17, Appl
33	16.2	77.1	471	4	US-09-996-243-393 Sequence 393, App
34	16.2	77.1	480	4	US-09-118-554-56 Sequence 56, Appl
35	16.2	77.1	480	4	US-09-118-627-56 Sequence 56, Appl
36	16.2	77.1	480	4	US-09-602-877A-56 Sequence 56, Appl
37	16.2	77.1	550	3	US-09-247-155-41 Sequence 41, Appl
38	16.2	77.1	578	4	US-08-998-416-148 Sequence 148, App
39	16.2	77.1	578	4	US-09-602-877A-95 Sequence 95, Appl
40	16.2	77.1	688	1	US-08-139-937-9 Sequence 9, Appl1
41	16.2	77.1	688	5	PCT-US93-11310-9 Sequence 9, Appl1
42	16.2	77.1	975	6	5340934-10 Patent No. 5340934
43	16.2	77.1	1539	6	5340934-9 Patent No. 5340934
44	16.2	77.1	1539	4	US-09-134-001C-1512 Sequence 1512, Ap
45	16.2	77.1	1677	2	US-08-684-101-1 Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-485-657A-19/c
Sequence 19, Application US/08485657A
Patent No. 5942389
GENERAL INFORMATION:
APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs
TYPE: nucleic acid
STRANDBESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
US-08-485-657A-19
Query Match 100.0%; Score 21; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAGCAGCAGGTTTCATCAT 21
|||||

73 CAGCAGCAGAGCTTTCATCAT 53

LT 2

9-366-380-19/c
Sequence 19, Application US/09366380
Item No. 6541603

GENERAL INFORMATION:
APPLICANT: Kirshling, Deborah J
APPLICANT: Gudkov, Andrei

TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,380

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,900

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: No. 6541603nan, Kevin E
REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002

TELEX:
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA

9-366-380-19
Query Match 100.0%; Score 21; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.96;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
73 CAGCAGCAGAGCTTTCATCAT 53

US95-02303-18/c
Sequence 18, Application PC/TUS9502303
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 181 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA

PCT-US95-02303-18
Query Match 100.0%; Score 21; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
73 CAGCAGCAGAGCTTTCATCAT 53

RESULT 4

US-08-485-657A-14/c
Sequence 14, Application US/08485657A
Patent No. 5942389

GENERAL INFORMATION:
APPLICANT: Kirshling, Deborah J
APPLICANT: Gudkov, Andrei

TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A

FILING DATE: 07-JUN-1995
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: No. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002

TELEX:
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA

US-08-485-657A-14
Query Match 100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATCAT 21
87 CAGCAGCAGAGCTTTCATCAT 67

US-08-485-657A-14

US-08-485-657A-14

RESULT 5

S-09-366-380-14/C

Sequence 14, Application US/09366380
Patent No. 6541603

GENERAL INFORMATION:

APPLICANT: Kirschling, Deborah J

APPLICANT: Gudkov, Andrei

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Genes and Genetic Elements Associated

TITLE OF INVENTION: with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSER: McDonnell Boehnen Hulbert & Berghoff

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/366,380

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/199,900

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6541603man, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: CDNA

-09-366-380-14

Query Match 100.0%; Score 21; DB 4; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21

87 CAGCAGCAGAGCTTCATCAT 67

SULT 6

T-US95-02303-14/C

Sequence 14, Application PC/TUS9502303

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Genes and Genetic Elements Associated

TITLE OF INVENTION: with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02303

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-02303-14

Query Match

Best Local Similarity 100.0%; Score 21; DB 5; Length 195;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21

87 CAGCAGCAGAGCTTCATCAT 67

RESULT 7

US-09-659-791A-3/C

Sequence 3, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 3

LENGTH: 1648

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (53) ... (1402)

US-09-659-791A-3

Query Match 100.0%; Score 21; DB 4; Length 1648;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21

73 CAGCAGCAGAGCTTCATCAT 53

Db

Db

Db

US-09-659-791A-13/C

Sequence 13, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 13

LENGTH: 1651

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (199) ... (1545)

US-09-659-791A-13

Query Match 100.0%; Score 21; DB 4; Length 1651;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21

216 CAGCAGCAGAGCTTCATCAT 196

Db

JULT 9
 -09-659-791A-12/c
 Sequence 12, Application US/09659791A
 Patent No. 6383808
 GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
 APPLICANT: Susan M. Pfeifer
 TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
 FILE REFERENCE: RTS-0156
 CURRENT APPLICATION NUMBER: US/09/659,791A
 CURRENT FILING DATE: 2000-09-11
 NUMBER OF SEQ ID NOS: 90
 SEQ ID NO 12
 LENGTH: 7610
 TYPE: DNA
 ORGANISM: Homo sapiens
 NAME/KEY: unsure
 LOCATION: 5461
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 5462
 OTHER INFORMATION: unknown
 -09-659-791A-12
 Query Match
 Best Local Similarity 100.0%; Score 21; DB 4; Length 7610;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CAGCAGCAGAGTCTTCATC 21
 5558 CAGCAGCAGAGTCTTCATC 5538
 JULT 10
 -08-950-925-1/c
 Sequence 1, Application US/08950925
 Patent No. 6072040
 GENERAL INFORMATION:
 APPLICANT: Dave, Kirti I.
 APPLICANT: Botyanszki, Janos
 APPLICANT: Sincar, Eva
 TITLE OF INVENTION: Stabilized Conjugates of Uncomplexed
 TITLE OF INVENTION: Subunits of Multimeric Proteins
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/950,925
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Axford, Laurie A
 REGISTRATION NUMBER: 35,053
 REFERENCE/DOCKET NUMBER: 32260-20004.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792

TELEX: 706141
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 633 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...630
 OTHER INFORMATION:
 US-08-950-925-1
 Query Match
 Best Local Similarity 82.9%; Score 17.4; DB 3; Length 633;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCAGCAGAGTCTTCATC 19
 DB 162 CAGCAGCAGAGTCTTCAGC 144
 RESULT 11
 US-09-565-286-1/c
 Sequence 1, Application US/09565286
 Patent No. 6491923
 GENERAL INFORMATION:
 APPLICANT: Dave, Kirti I.
 APPLICANT: Botyanszki, Janos
 APPLICANT: Sincar, Eva
 TITLE OF INVENTION: STABILIZED CONJUGATES OF UNCOMPLEXED
 TITLE OF INVENTION: SUBUNITS OF MULTIMERIC PROTEINS
 FILE REFERENCE: 35574-22004.10
 CURRENT APPLICATION NUMBER: US/09/565,286
 CURRENT FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: 08/950,925
 PRIOR FILING DATE: 1997-10-15
 PRIOR APPLICATION NUMBER: 08/730,111
 PRIOR FILING DATE: 1996-10-15
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 633
 TYPE: DNA
 ORGANISM: homo sapien
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(633)
 US-09-565-286-1
 Query Match
 Best Local Similarity 82.9%; Score 17.4; DB 4; Length 633;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCAGCAGAGTCTTCATC 19
 DB 162 CAGCAGCAGAGTCTTCAGC 144
 RESULT 12
 US-08-961-858-1/c
 Sequence 1, Application US/08961858
 Patent No. 5834210
 GENERAL INFORMATION:
 APPLICANT: Liu, Shigui
 APPLICANT: Shi, Qimei
 TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue, 4th Floor
 CITY: Hackensack
 STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,858

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

3-08-961-858-1

Query Match

Best Local Similarity 82.9%; Score 17.4; DB 2; Length 651;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATC 19

180 CAGCAGCAGAGCTTTCAGC 162

RESULT 13

1-08-961-858-3/c

Sequence 3, Application US/08961858

Patent No. 5834210

GENERAL INFORMATION:

APPLICANT: Liu, Shigu

APPLICANT: Shi, Qinhui

TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,858

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: native form
HYPOTHETICAL: NO
US-08-961-858-3

Query Match

Best Local Similarity 82.9%; Score 17.4; DB 2; Length 651;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATC 19

180 CAGCAGCAGAGCTTTCAGC 162

RESULT 14

US-09-089-593-1/c

Sequence 1, Application US/09089593

Patent No. 6060278

GENERAL INFORMATION:

APPLICANT: Liu, Shigu

APPLICANT: Shi, Qinhui

TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/089,593

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,858

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

US-09-089-593-1

Query Match

Best Local Similarity 82.9%; Score 17.4; DB 3; Length 651;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTTCATC 19

180 CAGCAGCAGAGCTTTCAGC 162

SULT 15
-09-089-593-3/c
Sequence 3, Application US/09089593
Patent No. 6060278
GENERAL INFORMATION:

APPLICANT: Liu, Shigui
APPLICANT: Shi, Qiwel
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSER: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,593
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,858

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 651 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

DESCRIPTION: native form

HYPOTHETICAL: NO

-09-089-593-3

Query Match 82.9%; Score 17.4; DB 3; Length 651;

Best Local Similarity 94.7%; Pred. No. 45;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATC 19

|||||
180 CAGCAGCAGAGTCTTCAGC 162

Search completed: November 8, 2003, 01:50:57
Time: 71 secs

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nucleic - nucleic search, using sw model

on: November 8, 2003, 00:41:58 ; Search time 256 Seconds

(without alignments)
221.438 Million cell updates/sec

le: US-09-944-326-4

fect score: 21

quence: 1 cagcagcagagcttcacat 21

ring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

urched: 2552756 seqs, 1349719017 residues

al number of hits satisfying chosen parameters: 5105512

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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:abase :
N:Geneseg_19Jun03:*
1: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1985.DAT:*
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8: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1988.DAT:*
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11: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1997.DAT:*
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20: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA2001A.DAT:*
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24: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneeq/geneeqn-emb1/NA2003.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length DB	ID	Description
1	21	100.0	21	AAA94226	Human testosterone
2	21	100.0	195	AAT00416	Genetic suppressor
3	21	100.0	275	AAC06940	Human secreted pro
4	21	100.0	395	AA94824	Human ovarian can
5	21	100.0	396	AB703091	Human ovarian carc
6	21	100.0	396	ABL48774	Ovarian carcinoma
7	21	100.0	491	AAC03751	Human secreted pro
8	21	100.0	512	AAV89150	EST clone CGI. HO

C	9	21	100.0	572	20	AAZ42136
C	10	21	100.0	704	24	ABO56105
C	11	21	100.0	922	21	AAA43857
C	12	21	100.0	1024	25	AB283527
C	13	21	100.0	1568	22	AA549448
C	14	21	100.0	1589	24	AB578654
C	15	21	100.0	1648	24	ABN99656
C	16	21	100.0	1651	12	AAQ11503
C	17	21	100.0	1651	24	ABN99666
C	18	21	100.0	1678	22	AAH23086
C	19	21	100.0	1712	24	AB578651
C	20	21	100.0	7610	24	ABN99665
C	21	18.4	87.6	215561	24	ABN1527
C	22	17.8	84.8	50	20	AAZ42790
C	23	17.8	84.8	366	25	ABX35023
C	24	17.8	84.8	377	25	ABX38693
C	25	17.8	84.8	379	25	ABX41456
C	26	17.8	84.8	389	25	ABX48928
C	27	17.8	84.8	413	25	ABX37325
C	28	17.8	84.8	414	25	ABX37324
C	29	17.8	84.8	416	25	ABX45607
C	30	17.8	84.8	416	25	ABX43344
C	31	17.8	84.8	417	17	AAT64832
C	32	17.8	84.8	418	17	AAT64834
C	33	17.8	84.8	426	17	AAT64833
C	34	17.8	84.8	426	25	ABX40866
C	35	17.8	84.8	446	21	AAC42717
C	36	17.8	84.8	448	21	AAC10235
C	37	17.8	84.8	460	17	AAT64831
C	38	17.8	84.8	520	24	AA46602
C	39	17.8	84.8	552	23	ABL10237
C	40	17.8	84.8	960	21	AAC45936
C	41	17.8	84.8	963	21	AAC42693
C	42	17.8	84.8	1201	21	AAC45344
C	43	17.8	84.8	2304	22	AA545136
C	44	17.8	84.8	2445	25	ACC46350
C	45	17.8	84.8	3050	23	ABL10236

ALIGNMENTS

```

RESULT 1
AAA94226
ID AAA94226 standard; DNA; 21 BP.
XX
AC AAA94226;
XX
DT 12-JAN-2001 (first entry)
XX
DB Human testosterone-repressed prostate message-2 antisense oligo #2.
XX
KW Human: testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
WO2000049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000MO-US04875.
XX
PR 26-FEB-1999; 99US-0121726.
XX
PA (UTBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX
DR WPI; 2000-533132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene -

```


Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
|||||
128 CAGCAGCAGAGTCTTCATCAT 108

3ULF 4
794824/C
AAP94824 standard; cDNA; 396 BP.

AAP94824;

23-MAY-2001 (first entry)

Human ovarian cancer associated coding sequence SEQ ID NO: 15.

Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

Homo sapiens.

MO200118046-A2.

15-MAR-2001.

08-SEP-2000; 2000MO-US24827.

10-SEP-1999; 99US-0394374.

01-MAY-2000; 2000US-0561778.

15-AUG-2000; 2000US-0640173.

07-SEP-2000; 2000US-0656668.

(CORI-) CORIXA CORP.

Xu J, Stolk JA;

WPI; 2001-211395/21.

Claim 18; Page 120; 1899p; English.

Isolated polypeptides associated with ovarian carcinomas, and the nucleic acids that encode them, useful for the prevention diagnosis and treatment of ovarian cancers.

The present invention provides a number of coding sequences and proteins, the over-expression of which is associated with ovarian carcinoma/cancer. These can be used in the diagnosis, treatment and prevention of ovarian cancer, optionally by gene therapy or in the form of a vaccine. The present sequence is an example of one of these sequences.

Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

Best Local Similarity 100.0%; Score 21; DB 22; Length 396;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
|||||
79 CAGCAGCAGAGTCTTCATCAT 59

ULF 5

03091/C
ABT03091 standard; cDNA; 396 BP.

ABT03091;

05-SEP-2002 (first entry)

Human ovarian carcinoma associated coding sequence SEQ ID NO: 15.

Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KM cytosolic; gene; ss.

XX Homo sapiens.

OS WO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Moleah DA;

XX WPI; 2002-500186/53.

XX Example 1; Page 117; 197p; English.

XX The present invention provides human ovarian cancer associated proteins

XX and coding sequences. The sequences can be used in the diagnosis and

XX treatment of ovarian cancers. The present sequence is a coding sequence

XX of the invention.

XX Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

XX Query Match 100.0%; Score 21; DB 24; Length 396;

XX Best Local Similarity 100.0%; Pred. No. 5.7;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCAGCAGAGTCTTCATCAT 21
|||||
Db 79 CAGCAGCAGAGTCTTCATCAT 59

RESULT 6

ABL48774/C

XX ABL48774 standard; cDNA; 396 BP.

XX ABL48774;

XX 18-JUN-2002 (first entry)

XX Ovarian carcinoma sequence isolate 23657.1.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

XX ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOLK/) STOLK J A.

XX (ALGAT) ALGATE P A.

(FLIN/) FLING S P.

Xu J, Stolk JA, Algate PA, Fling SP;

WPI; 2002-171027/22.

Ovarian tumour polypeptide and polynucleotide useful in diagnosis, prevention and/or treatment of cancer, especially ovarian cancer

Example 1; Page 43; 131pp; English.

The invention relates to ovarian tumour polynucleotides and polypeptides that may be utilised in cancer therapy, for example in a vaccine or gene therapy. Polypeptides and polynucleotides of the invention are useful for detecting a cancer in a patient, for stimulating and/or expanding T-cells specific for a tumour protein, and for inhibiting the development of a cancer in a patient. They are also useful for stimulating an immune response in a patient, and for treating a cancer in a patient and for determining the presence of a cancer in a patient. The isolated polynucleotides of the invention are useful for their ability to selectively form duplex molecules with complementary stretches of the entire desired gene or gene fragments, and for designing and preparing ribozyme molecules for inhibiting expression of tumour polypeptides in tumour cells. Polypeptides and polynucleotides of the invention are also useful in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. The sequences given in records ABL48760-ABL48956 represent polynucleotides encoding ovarian carcinoma proteins.

Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;

Very Match 100.0%; Score 21; DB 24; Length 396;
Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
|||||
79 CAGCAGCAGAGCTTCATCAT 59

LT 7
3751/C
AAC03751 standard; cDNA; 491 BP.

AAC03751;
06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 3749.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000BP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI; 2000-500381/45.

P-PSDB; AAG03745.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 3749; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNA encoding secreted proteins. An ORF has been identified within the
CC mRNA encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors.

XX Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;

Query Match 100.0%; Score 21; DB 21; Length 491;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
|||||
Db 128 CAGCAGCAGAGCTTCATCAT 108

RESULT 8
AAV89150/C
ID AAV89150 standard; cDNA; 512 BP.

XX AAV89150;

DT 15-FEB-1999 (first entry)
DE EST clone CG1.

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
KW gene therapy; ss.

XX Homo sapiens.

PN MO9845436-A2.

XX 15-OCT-1998.

XX 10-APR-1998; 98MO-US06955.

XX 10-APR-1997; 97US-0838821.

XX (GENY) GENNETICS INST INC.

PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;

XX WPI; 1999-070077/06.

PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries.

PS Claim 1; Page 126; 618pp; English.

XX The present sequence represents a human expressed sequence tag (EST).
XX The polynucleotide, which is a secreted EST, and the encoded protein
CC are predicted to have useful biological activities which would make
CC them suitable for treating, preventing or ameliorating medical
CC conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional activity, immune

stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.

Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 512;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
|||
55 CAGCAGCAGAGTCTTCATCAT 35

HLT 9
42136/c
AA242136 standard; cDNA; 572 BP.

AA242136;

31-JAN-2000 (first entry)

Human normal bladder tissue cDNA derived EST 15.

Human; bladder; treatment; EST; expressed sequence tag; cytostatic; cancer; gene therapy; ss.

Homo sapiens.

DE19818620-A1.

28-OCT-1999.

21-APR-1998; 98DE-1018620.

21-APR-1998; 98DE-1018620.

(META-) METAGEN GBS GENOMFORSCHUNG MBH.

Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E,

WPI; 1999-602416/52.

New polypeptides and their nucleic acids, useful for treatment of bladder tumour and identification of therapeutic agents

Claim 3; Page 158; 366pp; German.

This invention describes novel polypeptide fragment sequences (I) and their encoding nucleic acids (II) which are highly expressed in normal bladder tissue and have cytoskeletal activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, therapy vectors, or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different libraries representing different parts of the same unknown gene. Distorting the estimated frequency of occurrence in a particular tissue. AA242132-242248 represent EST fragments derived from a human normal bladder tissue cDNA library which encode the protein fragments represented in AA60323-Y60591.

Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other;

Query Match

100.0%; Score 21; DB 20; Length 572;

Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
|||
Db 196 CAGCAGCAGAGTCTTCATCAT 176

RESULT 10
ABQ56105/c
ID ABQ56105 standard; cDNA; 704 BP.

XX ABQ56105;

AC 22-AUG-2002 (first entry)

XX Human ovarian antigen HSPH41 cDNA, SEQ ID NO:1985.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX antiinflammatory; gynaecological; reproductive; gene; ss.

OS Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX P-PSDB; ABP43028.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases

PS Claim 1; SEQ ID NO 1985; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP41328) and to cDNAs encoding them (ABQ54131-ABQ56105), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigen
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders,
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which

modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 704 BP; 180 A; 197 C; 199 G; 121 T; 7 other;

Query Match 100.0%; Score 21; DB 24; Length 704;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 |||||
 149 CAGCAGCAGAGCTTCATCAT 129

LT 11

3857/c
 AAA43857 standard; cDNA; 922 BP.

AAA43857;

21-AUG-2000 (first entry)

Human secreted expressed sequence tag SEQ ID NO:432.

Human; mouse; chicken; rat; secreted expressed sequence tag; SEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiaesthetic; vulnery; antiparkinsonian; antitumor; osteoprotective; neuroprotective; nootropic; antiproliferative; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vasculin; autoimmune diabetes; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.

Homo sapiens.

WO200021991-A1.

20-APR-2000.

15-OCT-1999; 99MO-US24206.

15-OCT-1998; 98US-0104436.

(GENY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C, Merberg D, Treacy M, Bowman MR;

WPI; 2000-317938/27.

Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -

Claim 1; Page 316; 803pp; English.

AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on

CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antitumor; osteoprotective; neuroprotective;
 CC nootropic; antiparkinsonian; antiproliferative; cerebroprotective;
 CC anticonvulsant; and antidepressant. The SESTs can be used for gene
 CC therapy and in vaccines. The SESTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.

SO Sequence 922 BP; 243 A; 265 C; 244 G; 166 T; 4 other;

Query Match 100.0%; Score 21; DB 21; Length 922;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
 |||||
 DB 52 CAGCAGCAGAGCTTCATCAT 32

RESULT 12

AB283527/c
 ID AB283527 standard; cDNA; 1024 BP.

XX AB283527;

DT 14-MAY-2003 (first entry)

XX Toxicologically relevant human nucleotide sequence #686.

XX Toxicologically relevant gene; toxicological response; gene; ss.

OS Homo sapiens.

XX WO2003016500-A2.

PN 27-FEB-2003.

PD 16-AUG-2002; 2002MO-US26514.

PF 16-AUG-2001; 2001US-313080P.

PR (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Neft RE, Dunn RT, Adkins K, Pickett GG, Klier LD, Schmeisler K;

PI Alen P;

DR WPI; 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening
 XX of drugs, comprises comparing the expression profile of one or more
 XX human toxic response genes to a reference gene expression profile
 XX indicative of toxicity -

PS Claim 1; Page 232; 455pp; English.

CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also

described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in AB282842 to AB284764, or their fragments of at least 20 nucleotides, or homologues; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals.

Sequence 1024 BP; 262 A; 299 C; 278 G; 185 T; 0 other;

Query Match 100.0%; Score 21; DB 25; Length 1024;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
|||||
68 CAGCAGCAGAGCTTCATCAT 48

SU13
S44948/c
AAS44948 standard; cDNA; 1568 BP.

AAS44948;

18-DEC-2001 (first entry)

cDNA encoding novel human secretory protein, Seq ID No 29.

Human, secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

Homo sapiens.

NO200166689-A2.

13-SEP-2001.

05-MAR-2001; 2001MO-US04942.

07-MAR-2000; 2000US-0519705.
19-MAY-2000; 2000US-0574454.
17-JUN-2000; 2000US-0596193.
14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
20-OCT-2000; 2000US-0693267.

(HYSS-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P, Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
WPI, 2001-589934/66.
P-PSDB; AA028048.

PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders -
PS Claim 1; SEQ ID No 29; 107bp; English.

XX The invention relates to novel isolated human secreted polypeptides (I),
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
CC involved in increasing haematopoiesis, stem cell survival, bone growth
CC and remodelling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC or lymphoid cell disorders, platelet disorders and is useful for treating myeloid
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions,
CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
CC disorders, or periodontal disease. Furthermore, (I) is also useful for
CC gut protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAS44920-AAS45295 represent novel human secreted protein
CC coding sequences of the invention.

XX Sequence 1568 BP; 386 A; 456 C; 434 G; 292 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 1568;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGCTTCATCAT 21
|||||
Db 90 CAGCAGCAGAGCTTCATCAT 70

RESULT 14

AB578654/c

ID AB578654 standard; cDNA; 1589 BP.

XX AB578654;

DT 16-DEC-2002 (first entry)

XX Human cDNA encoding CGDD12, INCTB 7503618CB1.
XX Human; ss; gene; cell growth; differentiation; death; CGDD; cancer;
XX cell proliferative disorder; arteriosclerosis; atherosclerosis;
XX cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
XX polycythaemia vera; primary thrombocytopenia; developmental disorder;
XX renal tubular acidosis; anaemia; mental retardation; epilepsy; AIDS;
XX neurological disorder; Alzheimer disease; Parkinson's disease; asthma;
XX reproductive disorder; infertility; autoimmune disorder; gout; allergy;
XX autoimmune thyroiditis; acquired immunodeficiency syndrome; uveitis;
XX autoimmune thyroiditis; contact dermatitis; Crohn's disease; infection;
XX multiple sclerosis; glomerulonephritis; irritable bowel syndrome;
XX rheumatoid arthritis; osteoarthritis; osteoporosis; pancreatitis;

Homo sapiens.

MO200272830-A2.

19-SEP-2002.

08-FEB-2002; 2002MO-US03715.

09-FEB-2001; 2001US-26811P.

23-FEB-2001; 2001US-271175P.

08-MAR-2001; 2001US-274503P.

09-MAR-2001; 2001US-274552P.

(INCY-) INCYTE GENOMICS INC.

Yue H, Yao MG, Ison CH, Lu Y, Warren BA, Elliott VS, Baughn MR, Ding L, Xu Y, Gietzen KJ, Tang TY, Lal PG, Dugan BM, Burford N, Lu DAM, Richardson TW, Tran UK, Khare R, Walla NK;

MP1: 2002-72356/78.
P-PSDB; ABG97361.

New human proteins associated with cell growth, differentiation and death, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), cancer, atherosclerosis or hepatitis

Claim 5; Page 180-181; 181pp; English.

The invention relates to an isolated polypeptide comprising CGDD1-12 (cell growth, differentiation and death), a naturally occurring amino acid sequence at least 90% identical to CGDD, a biologically active fragment or an immunogenic fragment. Also included are the polynucleotides encoding CGDD1-12, a recombinant polynucleotide comprising a promoter sequence operably linked to the CGDD polynucleotide, a cell transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, anti-CDD antibody, screening for compounds which bind to/modulate or are anti/agonists of CGDD or alter the expression of CGDD polynucleotide and a CGDD polynucleotide microarray.

The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CGDD, particularly cell proliferative (e.g. atherosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS, (acquired immunodeficiency syndrome) allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis, uveitis, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections). They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with CGDD. The present sequence encodes a CGDD protein.

Sequence 1589 BP; 407 A; 421 C; 466 G; 295 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1589;
Best Local Similarity 100.0%; Pred. No. 6.8;
atches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
|||||
CAGCAGCAGAGCTTCATCAT 78

UUT 15

ABN99656/C
ID ABN99656 standard; DNA; 1648 BP.

AC ABN99656;

XX 16-AUG-2002 (first entry)

XX Human clusterin gene sequence 1.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;

XX hypercholesterolemia; cardiovascular disorder; ds;

XX hyperproliferative disorder; hyperlipidemic disorder.

XX Homo sapiens.

XX MO200222635-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001MO-US28235.

XX 11-SEP-2000; 2000US-0659791.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;

XX MP1: 2002-404805/43.

XX P-PSDB; AAO15039.

PT Novel antisense compound targeted to nucleic acid molecule encoding

PT clusterin, useful for treating animal having disease associated with

PT clusterin such as hyperlipidemic disorder, cardiovascular disorder

XX Example 13; Page 89-92; 125pp; English.

CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a human clusterin gene sequence.

SQ Sequence 1648 BP; 408 A; 488 C; 440 G; 312 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1648;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
|||||
DB 73 CAGCAGCAGAGCTTCATCAT 53

Search completed: November 8, 2003, 00:51:22
Job time : 258 secs

GenCore version 5.1.6
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Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

nucleic - nucleic search, using sw model

on: November 8, 2003, 00:45:43 ; Search time 1410 Seconds

(without alignments)
609.292 Million cell updates/sec

le: US-09-944-326-4

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oring cable: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

urched: 2888711 seqs, 20454813386 residues

al number of hits satisfying chosen parameters: 5777422

Hum DB seq length: 0
Hum DB seq length: 200000000

ic-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
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5: gb_ov:*
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7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
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41: gb_vl:*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	181	6 AR302789	AR302789 Sequence
C 2	21	100.0	195	6 AR302784	AR302784 Sequence
C 3	21	100.0	275	6 BD030685	BD030685 Sequence
C 4	21	100.0	396	6 AK093197	AK093197 Sequence
C 5	21	100.0	482	6 BD117323	BD117323 EST and e
C 6	21	100.0	491	6 BD027496	BD027496 Sequence
C 7	21	100.0	512	6 BD071299	BD071299 Secreted
C 8	21	100.0	1546	6 AK093399	AK093399 Homo sapi
C 9	21	100.0	1589	6 AK600212	AK600212 Sequence
C 10	21	100.0	1648	6 AR208704	AR208704 Sequence
C 11	21	100.0	1648	6 HMTTRPM2A	M64722 Human TRPM
C 12	21	100.0	1651	6 A21577	A21577 blood plasm
C 13	21	100.0	1651	6 AR208714	AR208714 Sequence
C 14	21	100.0	1651	6 HMTCLI	M25915 Human compl
C 15	21	100.0	1658	9 BC019588	BC019588 Homo sapi
C 16	21	100.0	1676	9 HSCSP40	X14723 Human SP-40
C 17	21	100.0	1678	6 AC202086	AC202086 Sequence
C 18	21	100.0	1684	9 BC010514	BC010514 Homo sapi
C 19	21	100.0	1712	6 AK600209	AK600209 Sequence
C 20	21	100.0	7610	6 AR208713	AR208713 Sequence
C 21	21	100.0	7610	6 HMTTRPM2A1	M63376 Human TRPM
C 22	21	100.0	134514	2 AC025192	AC025192 Homo sapi
C 23	21	100.0	175475	9 AF235104	AF235104 Homo sapi
C 24	21	100.0	234431	9 AF311103	AF311103 Homo sapi
C 25	21	100.0	334051	2 AC123374	AC123374 Rattus no
C 26	19.4	92.4	1636	4 DOGGR80	M55251 Dog glycop
C 27	19.4	92.4	1678	8 AF118852	AF118852 Oryctolag
C 28	18.4	87.6	3287	8 AF063235	AF063235 Pneumocys
C 29	18.4	87.6	23701	1 AE014247	AE014247 Streptoco
C 30	18.4	87.6	46099	6 AX602197	AX602197 Sequence
C 31	18.4	87.6	120871	2 AC140915	AC140915 Sequence
C 32	18.4	87.6	181889	10 AL845317	AL845317 Mouse DNA
C 33	18.4	87.6	199050	1 SAG766850	AL766850 Streptoco
C 34	18.4	87.6	300029	1 AE015936	AE015936 Clostridi
C 35	18.4	87.6	1632	4 PIGCCIMRA	M84639 Pig complem
C 36	17.8	84.8	264	5 AF023271	AF023271 NaJa sput
C 37	17.8	84.8	264	5 AF023272	AF023272 NaJa sput
C 38	17.8	84.8	278	5 NSU86588	NSU86588 NaJa sput
C 39	17.8	84.8	278	5 NSU86589	NSU86589 NaJa sput
C 40	17.8	84.8	278	5 NSU86591	NSU86591 NaJa sput
C 41	17.8	84.8	278	5 NSU86592	NSU86592 NaJa sput
C 42	17.8	84.8	278	5 NSU86593	NSU86593 NaJa sput
C 43	17.8	84.8	278	5 NSU86594	NSU86594 NaJa sput
C 44	17.8	84.8	278	5 NSU86595	NSU86595 NaJa sput
C 45	17.8	84.8	278	5 NSU86596	NSU86596 NaJa sput

ALIGNMENTS

RESULT 1
LOCUS AR302789 181 bp mRNA
DEFINITION Sequence 19 from patent US 6541603.
ACCESSION AR302789
VERSION AR302789.1 GI:31691276
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 181)
AUTHORS Kirschling,D.J., Gudkov,A. and Robinson,I.B.
TITLE Genes and genetic elements associated with sensitivity to
Platinum-based drugs
JOURNAL Patent: US 6541603-A 19 01-APR-2003;

SOURCE	Location/Qualifiers				
1	181				
1	/organism="unknown"				
3 COUNT	42 a 41 c 64 g 34 t				
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very Match	100.0%; Score 21; DB 6; Length 181;				
het Local Similarity	100.0%; Pred. No. 34;				
itches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
1 CAGCAGCAGACTTTCATCAT 21					
73 CAGCAGCAGACTTTCATCAT 53					
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12784/c					
IS AR302784	195 bp mRNA linear PAT 12-JUN-2003				
NTTON Sequence 14 from patent US 6541603.					
SSION AR302784					
ION AR302784..1 GI:31691271					
ORDS					
CE Unknown.					
GANISM Unclassified.					
RENCE 1 (bases 1 to 195)					
THORS Kirschling,D.J., Gudkov,A. and Roninson,I.B.					
TLE Genes and genetic elements associated with sensitivity to					
URNAL Platinum-based drugs					
URES Patent: US 6541603-A 14 01-APR-2003;					
source Location/Qualifiers					
1..195					
IN : COUNT 46 a 45 c 71 g 33 t					
ery Match	100.0%; Score 21; DB 6; Length 195;				
st Local Similarity	100.0%; Pred. No. 34;				
ches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
1 CAGCAGCAGACTTTCATCAT 21					
87 CAGCAGCAGACTTTCATCAT 67					
LT 3					
0685/c					
S BD030685	275 bp DNA linear PAT 27-AUG-2002				
NITION Sequence tag and encoded human protein.					
SSION BD030685..1 GI:22572427					
ION BD030685..1 GI:22572427					
ORDS JP 2001269182-A/6931.					
CR Homo sapiens (human)					
GANISM Homo sapiens					
Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
1 (bases 1 to 275)					
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.					
Sequence tag and encoded human protein					
Patient: JP 2001269182-A 6931 02-OCT-2001;					
GENSET					
OS Homo sapiens (human)					
PN JP 2001269182-A/6931					
PD 02-OCT-2001					
PF 24-FEB-2000 JP 2000118773					
PR 26-FEB-1999 US 60/122487					
PI JEAN BAUPUIST DUMAS MILNE EDWARDS,BIMERIC DUCLAIR,JEAN YVES					
JORDAN					
PC C12N15/09.C07K14/435.C07K16/18.C12N1/15.C12N1/19.C12N1/21, PC					
C12N5/10.					
PC C12P21/02.C12P21/08.C12O1/68//G06F17/30.C12N15/00.C12N5/00, PC					
G06F15/40					
CC					

FEATURES	Source	Key	Location/Qualifiers	Location/Qualifiers
1. 275	/organism="Homo sapiens"			
/mol_type="genomic DNA"				
/db_xref="taxon:9606"				
BASE COUNT	59 a	88 c	85 g	43 t
ORIGIN				
Query Match	100.0%;	Score 21;	DB 6;	Length 275;
Best Local Similarity	100.0%;	Pred. No. 33;		
Matches	21;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
OY	1 CAGCAGCAGAGCTTTCATCAT	21		
Db	79 CAGCAGCAGAGCTTTCATCAT	59		
RESULT 5				
BD117323/c				
LOCUS	BD117323	482 bp	DNA	linear
DEFINITION	EST and encoded human protein.			
ACCESSION	BD117323			
VERSION	BD117323.1	GI:232122227		
KEYWORDS	JP 2002010789-A/9400			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens.			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 482)			
AUTHORS	Edwards,J.B.D.M., Jobert,S. and Giordano,J.B.			
TITLE	EST and encoded human protein			
JOURNAL	Patent: JP 2002010789-A 9400 15-JAN-2002;			
GENSET CORP				
OS	Homo sapiens (human)			
PN	JP 2002010789-A/9400			
PD	15-JAN-2002			
PF	07-AUG-2000 JP 2000280989			
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1. 396	/organism="Homo sapiens"			
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Best Local Similarity	100.0%;	Pred. No. 32;		
Matches	21;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
OY	1 CAGCAGCAGAGCTTTCATCAT	21		
Db	79 CAGCAGCAGAGCTTTCATCAT	59		
RESULT 4				
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LOCUS	AX093197	396 bp	DNA	linear
DEFINITION	Sequence 15 from Patent WO0118046.			
ACCESSION	AX093197			
VERSION	AX093197.1	GI:13509646		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Xu,J. and Stolk,J.A.			
TITLE	Ovarian tumor sequences and methods of use therefor			
JOURNAL	Patent: WO 0118046-A 15 15-MAR-2001;			
CORIXA CORPORATION (US)				
FEATURES				
1. 396	/organism="Homo sapiens"			
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/db_xref="taxon:9606"				
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BASE COUNT	129 a	83 c	121 g	62 t
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Best Local Similarity	100.0%;	Pred. No. 32;		
Matches	21;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
OY	1 CAGCAGCAGAGCTTTCATCAT	21		
Db	79 CAGCAGCAGAGCTTTCATCAT	59		

PR 05-AUG-1999 US 60/147499
 PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN-EVE
 GORDANO
 PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
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 CC EST and encoded human protein
 FH Key Location/Qualifiers
 FT source 1. 482
 FT Location/Qualifiers
 1. 482
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 /mol_type="genomic DNA"
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US COUNT 148 a 107 c 150 g 76 t 1 others
 LGIN

Query Match 100.0%; Score 21; DB 6; Length 482;
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 |||||
 96 CAGCAGCAGAGCTTCATCAT 76

SUBMIT 6
 027496/c
 CTS BD027496 491 bp DNA linear PAT 27-AUG-2002
 DEFINITION Sequence tag and encoded human protein.
 REVISION BD027496.1 GI:22569238
 RSION JP 2001269182-A/3742
 TWOARDS Homo sapiens (human)
 TRACE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 491)
 Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
 Sequence tag and encoded human protein
 Patent: JP 2001269182-A 3742 02-OCT-2001;
 GENSET

MMENT OS Homo sapiens (human)

PN JP 2001269182-A/3742
 PD 02-OCT-2001
 PP 24-FEB-2000 JP 2000118773
 PR 26-FEB-1999 US 60/122487
 P1 JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
 P1 JORDAN
 PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
 C12N5/10,
 PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
 G06F15/40
 CC score 6.3
 CC seq LFPVGLLTMBSG/OV
 FH Key Location/Qualifiers
 FT CDS 108..455
 FT 819 peptide 108..161.
 FT Location/Qualifiers
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35 COUNT 149 a 114 c 149 g 78 t 1 others
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 1 CAGCAGCAGAGCTTCATCAT 21

DB 128 CAGCAGCAGAGCTTCATCAT 108
 |||||

RESULT 7
 BD071299/c
 LOCUS
 DEFINITION Secreted expressed sequence tags (ESTs).
 ACCESSION BD071299
 VERSION BD071299.1 GI:22616902
 KEYWORDS JP 2001519667-A/109.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 1 (bases 1 to 512)
 Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
 Tracy, M., Spaulding, V. and Agostino, M.J.
 Secreted expressed sequence tags (ESTs)
 Patent: JP 2001519667-A 109 23-OCT-2001;
 GENETICS INSTITUTE INC
 OS Unidentified
 PN JP 2001519667-A/109
 PD 23-OCT-2001
 PP 10-APR-1998 JP 1998543069
 PR 10-APR-1997 US 08/838821
 P1 KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
 DAVID MERBERG,
 PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
 C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
 Double;

COMMENT
 TITLE
 JOURNAL
 ORGANISM

FEATURES
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 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
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 DB 55 CAGCAGCAGAGCTTCATCAT 35

RESULT 8
 AK093399/c
 LOCUS
 DEFINITION Homo sapiens cDNA FLJ36080 f1s, clone TEST1019872, highly similar
 to CLUSTERIN PRECURSOR.
 ACCESSION AK093399
 VERSION AK093399.1 GI:21752259
 KEYWORDS oligo capping, f1s (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1546)
 Niishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
 Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
 Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
 Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
 Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
 Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
 Sugano, S., Nagahari, K., Maeno, Y., Negai, K. and Isegai, T.
 NEDO human cDNA sequencing project

REFERENCE
 AUTHORS
 TITLE

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1546)
 AUTHORS Isogai, T. and Yamamoto, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, Flj Project (HRI Team); 2-6-7
 Kazusa-Kamatazi, Kikarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

MEET MEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'-63'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.
 Location/Qualifiers
 source 1.1546
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TEST12019872"
 /cistype="cistype"
 /clone_lib="TEST12"
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GC COUNT 395 a 456 c 410 g 285 t
 Query Match 100.0%; Score 21; DB 9; Length 1546;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
 |||||
 99 CAGCAGCAGAGTCTTCATCAT 79

ULT 9
 00212/c
 AX600212 1589 bp DNA linear PAT 14-FEB-2003
 INTENTION Sequence 24 from Patent WO02072830.
 AX600212
 WORDS AX600212.1 GI:28400254
 RCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1
 Yue, H., Yao, M.G., Ison, C.H., Lu, Y., Warren, B.A., Elliott, V.S.,
 Baughn, M.R., Ding, L., Xu, Y., Gietzen, K.J., Tang, T.Y., Lal, P.G.,
 Duggan, B.M., Burford, N., Lu, D.A., Richardson, T.W., Tran, U.K.,
 Khare, R. and Wallis, N.K.
 Proteins associated with cell growth, differentiation, and death
 Patent: WO 02072830-A 24 19-SEP-2002;
 Incyte Genomics, Inc. (US)
 Location/Qualifiers
 source 1.1589
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /note="Incyte ID No: 7503618CB1"

GC COUNT 407 a 421 c 466 g 295 t
 Query Match 100.0%; Score 21; DB 6; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
 |||||
 98 CAGCAGCAGAGTCTTCATCAT 78

RESULT 10
 AR208704 1648 bp DNA linear PAT 20-JUN-2002
 LOCUS AR208704
 DEFINITION Sequence 3 from patent US 6383808.
 ACCESSION AR208704
 VERSION AR208704.1 GI:21509928
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1648)
 AUTHORS Monia, B.P. and Freiler, S.M.
 TITLE Antisense inhibition of clusterin expression
 JOURNAL Patent: US 6383808-A 3 07-MAY-2002;
 Location/Qualifiers
 source 1.1648
 /organism="unknown"
 ORIGIN 408 a 488 c 440 g 312 t

Query Match 100.0%; Score 21; DB 6; Length 1648;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
 |||||
 73 CAGCAGCAGAGTCTTCATCAT 53

RESULT 11
 HUMTRPM2A 1648 bp mRNA linear PRI 23-AUG-1996
 LOCUS HUMTRPM2A
 DEFINITION Human TRPM-2 mRNA, complete cds.
 ACCESSION M64722
 VERSION M64722.1 GI:339972
 KEYWORDS TRPM-2 protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (sites)
 Wong, P., Pineault, J., Lakin, J., Taillefer, D., Leger, J., Wang, C.
 and Tenniswood, M.
 Genomic organization and expression of the rat TRPM-2 (clusterin)
 gene, a gene implicated in apoptosis
 J. Biol. Chem. 268 (7), 5021-5031 (1993)
 MEDLINE 9318693
 PUBMED 7680346
 REFERENCE 2 (bases 1 to 1648)
 Wong, P., Taillefer, D., Lakin, J., Pineault, J., Chader, G. and
 Tenniswood, M.
 Molecular characterization of human TRPM-2/clusterin, a gene
 associated with sperm maturation, apoptosis and neurodegeneration
 Eur. J. Biochem. 221 (3), 917-925 (1994)
 MEDLINE 94237156
 PUBMED 8181474
 JOURNAL Original
 COMMENT source text: Human cDNA to mRNA.
 FEATURES
 source 1.1648
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 1.1648
 /gene="TRPM-2"
 53.1402
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 /codon_start=1
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 EIONAVNGVQIKTLIKTNERRKTLISNLEAKKKEDALNRRBSRTKLKIPVC
 NRTMALNBERCKPLKQTCNKFYARVCSGSGVIGRQLEETLWSSSPFTWNGDRIID
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gene
 CDS
 1.1648
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 53.1402
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 NRTMALNBERCKPLKQTCNKFYARVCSGSGVIGRQLEETLWSSSPFTWNGDRIID
 SLNDRQQTMLDVMQDHFSSASSIIDELEFQDRFTREPDYHYLPFSLPHRRPHR

polya_signal
 1627..1632
 /gene="TRPM-2"

JB COUNT 408 a 488 c 440 g 312 t
 (GIN

Query Match 100.0%; Score 21; DB 9; Length 1648;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 |||||
 73 CAGCAGCAGAGCTTCATCAT 53

MULT 12 1651 bp DNA linear PAT 26-JUL-1994
 .577/c
 US blood plasma component having a biological activity of inhibiting
 INITIATION cytolysis mediated by a cytolytic protein.
 SESSION A21577
 A21577 GI:579601

ORGANISM Homo sapiens (human)
 RCE
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1651)

REFERENCE CYTOLYSIS INHIBITOR PROTEINS (CLI) AND DNA SEQUENCES CODING FOR
 LITORS SAID PROTEINS
 JOURNAL Patent: WO 9105043-A 3 18-APR-1991;
 TURES Location/Qualifiers
 SOURCE 1..1651
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 199..1545
 /codon_start=1
 /product="blood plasma component having a biological
 activity of inhibiting cytolysis mediated by a cytolytic
 protein"
 /protein_id="CAA01560.1"
 /db_xref="GI:579602"
 /translation="MKTLIFVGLLWTBESGOVLDQTVSDNLEQMSNOGSKYVNE
 IONAVNGKQIKTLIKTERNEKRTLSLSEAKKKKEDALNTERESTKLELPGVON
 ETMAALMECKPCIKQCKFYARVCGSSGLVGRQLEBFLNQSPPYPMNNGRIDS
 LLENDROQTHLDMQDHPBSASSIIDELQDQRPTRBPOTYHYLPSPILPHRPHFP
 PPKSRIVRSIAMPSPYBPLNFHAMQFPLMIHEQAQMDIHFSAPAFQHPTEFIRE
 GDDRTVCRIIRNSSTGLCKMKQDCRCRILSVDCSTNNPSQAKRLREIDESQVAB
 RLTRKTNELKSYOMKMLNTSILBOLNBOFNWVSRILANTQGEDQYLLRTVVAASH
 SDSDVSGVTEVVVKLPDSDPITVTYVVEVSRKNPKMETVAERKALQEVKKHREE"

CDS

8 COUNT 405 a 481 c 447 g 318 t
 31N

Query Match 100.0%; Score 21; DB 6; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
 |||||
 216 CAGCAGCAGAGCTTCATCAT 196

TOT 13 1651 bp DNA linear PAT 20-JUN-2002
 38714/c
 25 AR208714 1651 bp DNA linear PAT 20-JUN-2002
 INITIATION Sequence 13 from patent US 6383808.
 SESSION AR208714

VERSION AR208714.1 GI:21509941

KEYWORDS
 SOURCE
 ORGANISM

REFERENCE 1 (bases 1 to 1651)

AUTHORS Monia,B.P. and Freiler,S.M.

TITLE Antisense inhibition of clusterin expression

JOURNAL Patent: US 6383808-A 13 07-MAY-2002;

FEATURES

source 1..1651
 /organism="unknown"

BASE COUNT 405 a 481 c 447 g 318 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1651;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21
 |||||
 DB 216 CAGCAGCAGAGCTTCATCAT 196

RESULT 14

HUMCLI/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

source

CDS

sig_peptide

mat_peptide

mat_peptide

mat_peptide

mat_peptide

mat_peptide

mat_peptide

mat_peptide

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mat_peptide

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mat_peptide

mat_peptide

mat_peptide

mat_peptide

mat_peptide

mat_peptide

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1 nucleic - nucleic search, using sw model

on on: November 8, 2003, 02:40:54 ; Search time 1968 Seconds
(without alignments)
259.347 Million cell updates/sec

file: US-09-944-326-4

reference score: 21

oring table: 1 cagcagcagcagcctcatcat 21

arched: 22781392 segs, 12152238056 residues

tal number of hits satisfying chosen parameters: 124404

num DB seq length: 0

ximum DB seq length: 50

et-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase :

EST.*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gse_hum:*
18: em_gse_hiv:*
19: em_gse_pln:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_phg:*
27: em_gse_vr1:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	14.8	70.5	46	9	AA916352
2	14.6	69.5	44	14	W25663
3	14	66.7	50	28	BH861678
4	13	61.9	21	28	AZ802584

5	13	61.9	41	28	BH908888
6	13	61.9	43	9	AA973632
7	13	61.9	48	29	AL948370
8	12.8	61.0	46	9	AL649065
9	12.8	61.0	50	9	AU107924
10	12.8	61.0	50	9	AU107925
11	12.8	61.0	50	9	AU107928
12	12.8	61.0	50	9	AU107929
13	12.6	60.0	39	29	AL760945
14	12.6	60.0	43	9	AI766391
15	12.6	60.0	46	9	AA561123
16	12.6	60.0	46	14	CB213634
17	12.6	60.0	50	9	AU105963
18	12.6	60.0	50	9	AU105967
19	12.6	60.0	50	9	AU105968
20	12.6	60.0	50	9	AU105972
21	12.6	60.0	50	9	AA566984
22	12.4	59.0	37	28	AZ797149
23	12.2	58.1	35	28	AZ332831
24	12.2	58.1	43	28	AZ610505
25	12.2	58.1	46	9	AA109083
26	12.2	58.1	49	9	AA052336
27	12.2	58.1	49	9	AA864073
28	12.2	58.1	50	9	AU104442
29	12.2	57.1	33	28	AZ305164
30	12.2	57.1	33	28	AZ318599
31	12.2	57.1	34	9	AA116347
32	12.2	57.1	34	12	BI246596
33	12.2	57.1	35	29	BX285461
34	12.2	57.1	40	28	BH910804
35	12.2	57.1	41	29	BZ586362
36	12.2	57.1	46	14	H92446
37	12.2	57.1	46	14	T74174
38	12.2	57.1	47	28	AZ772648
39	12.2	57.1	49	9	AI197165
40	12.2	57.1	49	28	AQ025388
41	12.2	57.1	49	29	BZ582545
42	12.2	57.1	49	29	DME545293
43	12.2	57.1	50	9	AU103332
44	12.2	57.1	50	9	AU103352
45	12.2	57.1	50	9	AU107277

ALIGNMENTS

RESULT 1
AA916352
LOCUS
DEFINITION
Ch80e11.61 NCI CGAP C08 Homo sapiens CDNA clone IMAGE:147356 3'
similar to TR:Q15347 Q15347 RAGA. [1] ; mRNA sequence.
AA916352
ACCESSION
AA916352
VERSION
AA916352.1 GI:3055744
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Bmerit-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.livl.gov/bbtp/image/image.html

AA916352 46 bp mRNA linear EST 14-APR-1998
Ch80e11.61 NCI CGAP C08 Homo sapiens CDNA clone IMAGE:147356 3'
similar to TR:Q15347 Q15347 RAGA. [1] ; mRNA sequence.
AA916352
ACCESSION
AA916352
VERSION
AA916352.1 GI:3055744
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

Trace considered overall poor quality
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 1.
Location/Qualifiers

1. 46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1473356"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: Colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Berto Soares and M. Fatima Bonaldo."

B COUNT 11 a 12 c 8 g 15 t

Query Match 70.5%; Score 14.8; DB 9; Length 46;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 18
|||||
20 CAGCAGCTTACCTTCAT 37

W25663 44 bp mRNA linear EST 25-NOV-1996
ZC6608.k1 Soares fetal heart, NBH19W Homo sapiens cDNA clone
IMAGE:327110.5 similar to gb:U15183_cdel HEAT SHOCK PROTEIN HSP
90-ALPHA (HUMAN); mRNA sequence.

W25663
W25663.1 GI:1303517
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 44)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Ritzkin, L., Rohlfsing, T., Soares, M., Tan, P., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LML; contact the IMGB Consortium (imgb@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 596 Std Error: 0.00
Seq primer: mob.RGA+ET
High quality sequence stop: 1.
Location/Qualifiers

1. 44
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:327110"
/sex="unknown"

/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBH19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASR COUNT 12 a 8 c 11 g 12 t 1 others

Query Match 69.5%; Score 14.6; DB 14; Length 44;
Best Local Similarity 81.0%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
|||||
26 CAGCAGTAGGCTTCATCTCAT 6

RESULT 3
BH861678/c
LOCUS
DEFINITION
SALK_087727 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_087727, genomic survey sequence.
BH861678
ACCESSION
BH861678.1 GI:22097004
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (chale crese)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 50)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, N., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shim, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers

1. 50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_087727"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASR COUNT 10 a 14 c 15 g 11 t

Query Match 66.7%; Score 14; DB 28; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.4e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3 CCAGCAGAGCTCTTC 16
 |||||
 41 CCAGCAGAGCTCTTC 28

SUBT 4
 KCS 802584
 INITIATION 21 bp DNA linear GSS 16-FEB-2001
 2M0061105R Mouse 10kb plasmid UGCM library Mus musculus genomic
 clone UGCG2M0061105 R, genomic survey sequence.
 A2802584
 REGION A2802584.1 GI:12954907
 WORDS GSS.
 ORIGIN Mus musculus (house mouse)
 MUS musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0061 row: 1 column: 05
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0061105"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /note="Vector: PWD2nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source
 8 a 7 c 3 g 3 t
 16 COUNT

ORIGIN
 Query Match 61.9%; Score 13; DB 28; Length 21;
 Best Local Similarity 76.2%; Pred. No. 4.1e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 1 CAGCAGCAGAGCTCTTCATCAT 21
 |||||
 1 CAGCAGCAGCATACATCATCAT 21

RESULT 5
 BH908888
 LOCUS
 DEFINITION 41 bp DNA linear GSS 04-SEP-2002
 SALK_051042.25.80.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_051042.25.80.x, genomic
 survey sequence.
 BH908888
 ACCESSION BH908888.1 GI:22721821
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 41)
 Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadri, N.,
 C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.
 A Sequence-indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single-pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At5g58140.
 Class: TDNA tagged.
 Location/Qualifiers
 1..41
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_051042.25.80.x"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES
 source
 1..41
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_051042.25.80.x"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
 8 a 11 c 9 g 12 t 1 others

ORIGIN
 Query Match 61.9%; Score 13; DB 28; Length 41;
 Best Local Similarity 76.2%; Pred. No. 5.9e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 1 CAGCAGCAGAGCTCTTCATCAT 21
 |||||
 19 CAGCAGGAGGATTTTACCAT 39

RESULT 6
 AA973632
 LOCUS
 DEFINITION 43 bp mRNA linear EST 17-JUN-1998
 co48b04.s1 NCI_CGAP Lys Homo sapiens cDNA clone IMAGE:1569391 3'
 similar to SW:XPB_CERRA P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E ;

Sequencing primer: SP6

This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

Location/Qualifiers

1. 46

/organism="Silurana tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TGae034101"

/dev_stage="gastrula (stages 10.5-13 mixed)"

/lab_name="XGC-gastrula"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA

was oligo dT primed from Sug of poly A+ RNA from stages

10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated

into pCS107 with EcoRI at the 5' end and NotI at the 3'

end."

ASB COUNT 10 a 14 c 11 g 11 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 9; Length 46;

Best Local Similarity 87.5%; Pred. No. 7.7e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 6 GCAGAGCTTCATCAT 21

21 GCCGCGCTTCATCAT 36

ESUT 9 50 bp mRNA linear EST 30-AUG-2001

OCUS AU107924 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

CCBSSION HRC02185, mRNA sequence.

ERSON AU107924 GI:13557446

CURCE EST.

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata

, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki

, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Location/Qualifiers

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC02185"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 21 g 4 t

2 AGCAGCAGAGCTTCA 17

Db 27 AGCAGCAGAGCTCCGA 42

RESULT 10

AU107925

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HS106916"

/clone_lib="Sugano Homo sapiens cDNA library"

10 a 15 c 19 g 6 t

27 AGCAGCAGAGCTCCGA 42

Query Match 61.0%; Score 12.8; DB 9; Length 50;

Best Local Similarity 87.5%; Pred. No. 8.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 AGCAGCAGAGCTTCA 17

27 AGCAGCAGAGCTCCGA 42

RESULT 11

AU107928

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

MENT Contact: Yuraka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuazuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ZRV62348"
/clone_id="Sugano Homo sapiens cDNA library"
15 c 20 g 5 c

SR COUNT 10 a 15 c 20 g 5 c

IGIN

Query Match 61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGCAGCAGAGTCTTCA 17
|||||
29 AGCAGCAGAGTCTTCA 44

SULT 12 50 bp mRNA linear EST 30-AUG-2001
107929
FINITION AUI07929 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV62402, mRNA sequence.
CESSION AUI07929
RSION AUI07929.1 GI:13557451
YWORDS EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isegaki, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yuraka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuazuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ZRV62402"
/clone_id="Sugano Homo sapiens cDNA library"
17 c 18 g 5 c

SE COUNT 10 a 17 c 18 g 5 c

IGIN

Query Match 61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 8.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGCAGCAGAGTCTTCA 17
|||||
29 AGCAGCAGAGTCTTCA 44

RESULT 13 39 bp DNA linear GSS 18-JUN-2002
AL760945
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-204B10-014508,
DEFINITION genomic survey sequence.
AL760945
ACCESSION AL760945.1 GI:21501350
VERSION
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
and Weishaar, B.
A pipeline for automated high-throughput generation of ESTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 39)
Rosso, M., Li, Y., Strizhov, N. and Weishaar, B.
Direct Submision
Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone ti037. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. 39
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-204B10-014508"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT 10 a 12 c 10 g 7 c

ORIGIN

Query Match 60.0%; Score 12.6; DB 29; Length 39;
Best Local Similarity 78.9%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 AGCAGCAGAGTCTTCA 20
|||||
38 AGCAGCAGAGTCTTCA 20

QY

Db

RESULT 14 43 bp mRNA linear EST 20-DEC-1999
AI766391/c
LOCUS wh61004.x1 NCI_CGAP Kid11 Homo sapiens cDNA clone IMAGE:238523 3'
DEFINITION similar to SW-COX2_HUMAN P00403 CYTOCHROME C OXIDASE POLYPEPTIDE II

```

SUBMIT 15
561123/c
CDS
FINITION
DEHYDROGENASE ;, mRNA sequence.
CROSSIN
RSION
YWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
; mRNA sequence.
AI766391
AI766391.1 GI:5232900
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
Tissue Procurement: Christopher Mookaluk, M.D., Ph.D., Michael R.
Bamert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
www-bio.linn.gov/bdtp/image/image.html
Trace considered overall poor quality
Insert Length: 641 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2385223"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/notes="Organ: Kidney; Vector: pRT7D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid1
was prepared, and 86 circles were made in vitro. Following HAP
pufication, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Patim Bernaldo."
10 a 5 c 21 g 7 t
58 COUNT
IGIN
Best Match 60.0%; Score 12.6; DB 9; Length 43;
Query Local Similarity 78.9%; Pred. No. 9, 1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1. CAGCAGCAGAGCTTCATC 19
2 CATCATCATGCTCTCATC 14
AA561123 46 bp mRNA linear EST 18-AUG-1997
VI4IC01.r1 Stratagene mouse skin (#937313) Mus musculus CDNA clone
IMAGE:974784 5' similar to TR:G972037 G972037 SCURCINATB
DEHYDROGENASE ;, mRNA sequence.
AA561123
AA561123.1 GI:2332588
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Marrta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

```

```

TITLE
JOURNAL
COMMENT
Getseil,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The Mashu-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
Mashu-HHMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINT ; contact the
IMAGS Consortium (info@image.lnl.gov) for further information.
M01:555512
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGS:974784"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_1kb="Stratagene mouse skin (#937113)"
/note="Organ: skin; Vector: plusscript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAAATCGACGACG 3' -3' adaptor
sequence: 5' CTCGAGTTTATTTTATTTT 3'."
BASE COUNT
11 a 11 c 15 g 9 t
ORIGIN
Query Match 60.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 78.9%; Pred. No. 9.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGTCTTCATC 19
|||||
Db 46 CAGCATCATGATTCGACG 28
|||||

```

```

Query Match          60.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 78.9%; Pred. No. 9.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAGCAGCAGAGTCTTCATC 19
        ||||| ||||| |||||
Db      46 CAGCATCAGATTCTGCAGC 28

```

Search completed: November 8, 2003, 03:50:17
Job time : 1973 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

1 nucleic - nucleic search, using sw model

on: November 8, 2003, 01:51:04 ; Search time 1422 Seconds

(without alignments)
604.151 Million cell updates/sec

File: US-09-944-326-4

Reference score: 21
1 cagcagcagagctctcatcat 21

Indexing table: IDENTITY NJC
Gapop 10.0 , Gapext 1.0

Indexed: 2888711 seqs, 2045481386 residues

total number of hits satisfying chosen parameters: 1316618

Minimum DB seq length: 0
Minimum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: GenBank

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_scs:*

12: gb_ey:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_scs:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_ay:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB ID	Description
1	16.2	77.1	32	6	AR274120
2	16.2	77.1	48	6	A76301
3	16.2	77.1	48	6	E01067
4	15.4	73.3	39	6	A08489
5	15.4	73.3	39	6	A12568
6	15.4	73.3	45	6	A05116
7	15.2	72.4	22	6	AX268965
8	14.8	70.5	27	6	AX118356
9	14.8	70.5	31	6	AR070079
10	14.8	70.5	31	6	AR258163
11	14.8	70.5	31	6	AK670795
12	14.6	69.5	48	6	A76303
13	14.4	68.6	39	6	A08490
14	14.4	68.6	39	6	A08491
15	14.4	68.6	39	6	A12569
16	14.4	68.6	39	6	A12570
17	14.2	67.6	20	6	AR085567
18	14.2	67.6	20	6	AR221110
19	14.2	67.6	22	6	AK697095
20	14.2	67.6	24	6	AR221229
21	14.2	67.6	26	6	AK697096
22	14.2	67.6	30	6	A70102
23	14.2	67.6	30	6	AR148235
24	14.2	67.6	30	6	AR204084
25	14.2	67.6	47	6	BD077090
26	14.2	67.6	47	6	AR291280
27	13.8	65.7	18	6	AR092800
28	13.8	65.7	31	6	A36373
29	13.8	65.7	37	6	AR070094
30	13.8	65.7	37	6	AR258178
31	13.8	65.7	37	6	AK670814
32	13.8	65.7	50	6	AX233374
33	13.6	64.8	20	6	AR230827
34	13.6	64.8	20	6	AR314013
35	13.6	64.8	20	6	BD064760
36	13.6	64.8	20	6	BD101829
37	13.6	64.8	23	6	AR234673
38	13.6	64.8	50	6	AR252583
39	13.6	64.8	50	6	AX080828
40	13.6	64.8	50	6	AX403425
41	13.4	63.8	20	6	AR221109
42	13.4	63.8	34	6	AR045234
43	13.2	62.9	18	6	I52286
44	13.2	62.9	18	6	AR085592
45	13.2	62.9	23	6	AX262444

ALIGNMENTS

RESULT 1
AR274120
LOCUS AR274120 32 bp
DEFINITION Sequence 6 from patent US 6504083.
ACCESSION AR274120
VERSION AR274120.1 GI:29706097
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Barbour,B., Meyer,T.B.C. and Saad,M.B.
TITLE Maize Gcs-2 promoters
JOURNAL Patent: US 6504083-A 6 07-JAN-2003;
FEATURES Location/Qualifiers

OY 4 CAGCAGTCTTCATCA 20
 |||||
Db 12 CAGCAGTCTTCACCA 28

```

SUTL 5
2568 A12568 39 bp DNA linear PAT 04-JAN-1994
TITLE Fragment of bovine somatotropin.
JOURNAL A12568
AUTHORS A12568.1 GI:488953
WORDS Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eumetazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 39)
REFERENCE
1 (bases 1 to 39)
TITLE ENHANCED BIOACTIVITY OF MAMMALIAN SOMATOTROPIN THROUGH SELECTIVE
DEAMINATION
JOURNAL Patent: WO 8701708-A 5 26-MAR-1987;
AUTHORS Location/Qualifiers
WORDS 1.39
ORGANISM="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
GIN 8 a 13 c 8 g 10 t
Query Match 73.3%; Score 15.4; DB 6; Length 39;
Best Local Similarity 94.1%; Pred. No. 1.9e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
4 CAGCAGAGCTTCATCA 20
12 CAGCAGAGCTTCACCA 28
SUTL 6
116 A05116 45 bp DNA linear PAT 04-MAY-1993
TITLE Oligonucleotide U7 for bovine growth hormone.
JOURNAL A05116
AUTHORS A05116.1 GI:345003
WORDS 1.45
ORGANISM="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
GIN 8 a 17 c 10 g 10 t
Query Match 73.3%; Score 15.4; DB 6; Length 45;
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
4 CAGCAGAGCTTCATCA 20
21 CAGCAGAGCTTCACCA 37
SUTL 7
68965 AX268965 22 bp DNA linear PAT 29-OCT-2001
TITLE Sequence 46 from Patent WO0175165.
JOURNAL AX268965
AUTHORS AX268965.1 GI:16541984
WORDS 1.22
ORGANISM="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
GIN 8 a 17 c 10 g 10 t
Query Match 70.5%; Score 14.8; DB 6; Length 27;
Best Local Similarity 84.2%; Pred. No. 3.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
2 AGCAGAGAGCTTCATCA 20
22 AGCAGAGAGCTTCATCA 4

```

```

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS Mcconlogue, L.C., Games, K.D., Yednock, T.A., Hua, T., Messersmith, B.
and Bard, P.
TITLE Screening markers and methods for neurodegenerative disorders
JOURNAL Patent: WO 0175165-A 46 11-OCT-2001;
WORDS Elan Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="forward primer 662P"
BASE COUNT 6 a 8 c 3 g 5 t
ORIGIN
Query Match 72.4%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 2.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCAGAGAGCTTCATCA 20
DB 2 CAGCAGAGAGCTTCATCA 21
RESULT 8
AX118356 27 bp DNA linear PAT 11-MAY-2001
LOCUS AX118356
DEFINITION Sequence 3479 from Patent WO0129262.
ACCESSION AX118356
VERSION AX118356.1 GI:14035307
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3479 26-APR-2001;
WORDS Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"
misc_feature 1..27
/note="n = C3 linker"
BASE COUNT 5 a 8 c 4 g 9 t 1 others
ORIGIN
Query Match 70.5%; Score 14.8; DB 6; Length 27;
Best Local Similarity 84.2%; Pred. No. 3.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGCAGAGAGCTTCATCA 20
DB 22 AGCAGAGAGCTTCATCA 4
RESULT 9
AR070079 31 bp DNA linear PAT 18-FEB-2000
LOCUS AR070079
DEFINITION Sequence 35 from patent US 5691716.
ACCESSION AR070079
VERSION AR070079.1 GI:7220967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)

```

Query Match	68.6%	Score 14.4;	DB 6;	Length 39;
Best Local Similarity	93.8%	Pred. No. 5.6e+04;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
4	CAGCAGAGCTTCATC	19		

|||||
12 CAGCAGAGCTTCAC 27

SULT 14
8491
CUS A08491 39 bp DNA linear PAT 22-JUL-1993
PINTION oligonucleotide 4.
CESSION A08491
RSION A08491.1 GI:413473
WORDS
URCE
ORGANISM synthetic construct
synthetic construct
artificial sequences.
PERENCE 1 (bases 1 to 39)
AUTHORS Harbourn,G.C., Hoogerheide,J.G. and Garlick,R.L.
TITLE Enhanced bioactivity of mammalian somatotropin through selective
deamidation
JOURNAL Patent: EP 0263206-A 7 13-APR-1988;
THE UPJOHN COMPANY
AUTHORS Location/Qualifiers
source 1. 39
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BE COUNT 8 a 11 c 10 g 10 t

Query Match 68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
4 CAGCAGAGCTTCATC 19
|||||
12 CAGCAGAGCTTCAC 27

ULT 15
3569
11569 39 bp DNA linear PAT 04-JAN-1994
INITIATION fragment of synthetic somatotropin.
TESSION A12569
BYON A12569 GI:491409
WORDS
RCR
ORGANISM synthetic construct
synthetic construct
artificial sequences.
ERENCE 1 (bases 1 to 39)
UTORS
TITLE
JOURNAL ENHANCED BIOACTIVITY OF MAMMALIAN SOMATOTROPIN THROUGH SELECTIVE
TURBS DEAMIDATION
source Patent: WO 8701708-A 6 26-MAR-1987;
1. 39
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BE COUNT 7 a 12 c 10 g 10 t
GIN
very Match 68.6%; Score 14.4; DB 6; Length 39;
est Local Similarity 93.8%; Pred. No. 5.6e+04;
atches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
4 CAGCAGAGCTTCATC 19
|||||
12 CAGCAGAGCTTCAC 27

rch completed: November 8, 2003, 03:17:13
time: 1424 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

M nucleic - nucleic search, using sw model

on on: November 8, 2003, 01:49:39 ; Search time 251 Seconds
(without alignments)
225.849 Million cell updates/sec

file: US-09-944-326-4

effect score: 21

sequence: 1 cagcagcagagcttcacat 21

scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

searched: 2552756 seqs, 1349719017 residues

total number of hits satisfying chosen parameters: 2467832

infimum DB seq length: 0

maximum DB seq length: 50

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	21	AAA94226
2	17.8	84.8	50	20	AAK24790
3	16.2	77.1	32	21	AAA09140
4	15.2	72.4	22	22	AAAI1024
5	15.2	72.4	22	22	AAAI5291
6	15.2	72.4	40	21	AAZ96146
7	14.8	70.5	33	24	ABQ80863
8	14.8	70.5	21	21	AAA94223

9	14.8	70.5	21	21	AAA94224	Human testosteron
10	14.8	70.5	27	22	AAH40683	Human testosteron
11	14.8	70.5	30	20	AAZ12445	Human testosteron
12	14.8	70.5	31	15	AAQ69972	Human testosteron
13	14.6	69.5	24	24	ABL61345	Human testosteron
14	14.6	69.5	33	24	ABK49118	Human testosteron
15	14.6	69.5	34	22	AAH79384	Human testosteron
16	14.6	69.5	44	20	AAK05964	Human testosteron
17	14.4	68.6	30	25	ABZ77331	Human testosteron
18	14.2	67.6	20	24	AAZ31857	Human testosteron
19	14.2	67.6	20	24	ABK69555	Human testosteron
20	14.2	67.6	22	21	AAK58494	Human testosteron
21	14.2	67.6	22	21	AAA37208	Human testosteron
22	14.2	67.6	22	22	AAK54314	Human testosteron
23	14.2	67.6	24	20	AAK08676	Human testosteron
24	14.2	67.6	24	22	AAK73404	Human testosteron
25	14.2	67.6	26	21	AAK58495	Human testosteron
26	14.2	67.6	26	21	AAA37209	Human testosteron
27	14.2	67.6	26	22	AAK54315	Human testosteron
28	14.2	67.6	30	20	AAK19511	Human testosteron
29	14.2	67.6	34	18	AAK6354	Human testosteron
30	13.8	65.7	18	21	AAZ57675	Human testosteron
31	13.8	65.7	28	24	ABK14351	Human testosteron
32	13.8	65.7	30	22	AAK28287	Human testosteron
33	13.8	65.7	31	14	AAK47780	Human testosteron
34	13.8	65.7	31	14	AAK47780	Human testosteron
35	13.8	65.7	36	22	AAK56649	Human testosteron
36	13.8	65.7	36	22	AAK56654	Human testosteron
37	13.8	65.7	36	22	AAK56656	Human testosteron
38	13.8	65.7	41	22	AAK28289	Human testosteron
39	13.8	65.7	50	22	AAK53508	Human testosteron
40	13.6	64.8	20	20	AAK55224	Human testosteron
41	13.6	64.8	20	22	AAK55666	Human testosteron
42	13.6	64.8	23	21	AAK69796	Human testosteron
43	13.6	64.8	24	14	ABK10729	Human testosteron
44	13.6	64.8	27	14	AAK40995	Human testosteron
45	13.6	64.8	32	20	AAK25040	Human testosteron

ALIGNMENTS

RESULT 1	AAA94226	standard; DNA; 21 BP.
ID	AAA94226	
AC	AAA94226;	
XX		
DT	12-JAN-2001	(first entry)
XX		
DB	Human testosteron-repressed prostate message-2	antitense oligo #2.
XX		
KW	Human; testosteron-repressed prostate message-2; TRPM-2; clusterin;	
KV	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200049937-A2.	
XX		
PD	31-AUG-2000.	
XX		
PP	25-FEB-2000; 2000WO-US04875.	
XX		
PR	26-FEB-1999; 99US-0121726.	
XX		
PA	(UTBR-) UNIV BRITISH COLUMBIA.	
XX		
PI	Gleavage M, Rennie PS, Miyake H, Nelson C;	
XX		
DR	WPI; 2000-533132/48.	
XX		
PT	Treating prostatic tumors and renal cancers by antisense inhibition of	
PT	the testosteron-repressed prostate messenger-2 gene.	

Claim 3; Page 36; 38pp; English.

The present sequence is an antisense oligonucleotide directed at the human testosterone-repressed prostate message-2 (TRPM-2), also known as clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to promote the regression of tumours, and oligonucleotides directed at human TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2 gene. These include prostate cancer, renal cell cancer and some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.

Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
1 CAGCAGCAGAGTCTTCATCAT 21

ULT 2
24790/c
AAx24790 standard; DNA; 50 BP.

AAx24790;

21-JUN-1999 (first entry)

Interleukin-18 binding protein splice variant IL-18BPA PCR primer.

Interleukin-18 binding protein; IL-18BP; IL-18BPA; splice variant; human; autoimmune disease; inflammation; diabetes; pancreatitis; rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis; psoriasis; inflammatory bowel disease; multiple sclerosis; ischemic heart disease; ischemic brain injury; gene therapy; PCR; primer; ss.

Synthetic.
Homo sapiens.

WO9909063-A1.

25-FEB-1999.

13-AUG-1998; 98MO-1100379.

22-JUL-1998; 98IL-0125463.

14-AUG-1997; 97IL-0121554.

27-AUG-1997; 97IL-0121639.

29-SEP-1997; 97IL-0121860.

06-NOV-1997; 97IL-0122134.

(YEDA) YEDA RES & DEV CO LTD.

Dinarello C, Kim SH, Novick D, Rubinstein M;

WPI; 1999-180975/15.

New interleukin-18 binding protein - useful for treating human diseases, including autoimmune disease and inflammation

Example 7; Page 39; 100pp; English.

The present sequence is a reverse primer that was used with a forward primer (see AAx24754) in the PCR amplification of the coding region of a cDNA clone (see AAx24749) coding for human interleukin-18 binding protein splice variant IL-18BPA (see AAx98004). The PCR products were cut with XbaI and cloned into the XbaI site of the pEF-BOS expression vector. IL-BP18a was expressed in transfected

CC COS7 cells. The invention provides IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity.
CC These can be used to treat conditions requiring the protein
CC (claimed), such as autoimmune diseases, type I diabetes, rheumatoid
CC arthritis, graft rejection, inflammatory bowel disease, sepsis,
CC multiple sclerosis, ischemic heart disease, ischemic brain injury,
CC chronic hepatitis, psoriasis, and chronic/acute pancreatitis.
XX

SO Sequence 50 BP; 13 A; 8 C; 13 G; 16 T; 0 other;

Query Match 84.8%; Score 17.8; DB 20; Length 50;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 42 CAGCAGCAGAGTCTTCATCAT 22

RESULT 3
AAA09140
ID AAA09140 standard; DNA; 32 BP.

XX AAA09140;

XX 10-AUG-2000 (first entry)

XX Gos-2 promoter gene-specific primer 1.

KW maize; promoter; actin-2; enolase; Gos-2; L41; gene expression;
KW regulation; plant transformation; primer; ss.

XX Zea mays.

XX WO200020571-A2.

XX 13-APR-2000.

XX 05-OCT-1999; 99MO-US23081.

XX 06-OCT-1998; 98US-0103294.

XX 05-NOV-1998; 98US-0107201.

XX (PION-) PIONEER HI-BRED INT INC.
XX (AGER-) AGERI AGRIC GENETIC ENG RES INST.

XX Barbour E, Meyer TE, Saad ME;

XX WPI; 2000-303763/26.

XX Novel maize promoters used for producing transgenic plants with
XX regulated expression of heterologous nucleotide sequences

XX Example 1; Page 26; 48pp; English.

CC Novel maize promoters (AAA09134-37) that drive expression of actin-2,
CC enolase, Gos-2 or L41, respectively, were isolated from genomic DNA
CC using PCR. The first round of PCR was performed on each DNA sample
CC using PCR. The first round of PCR was performed on each DNA sample with
CC Clontech primer API (AAA09138) and a gene-specific primer 1
CC (AAA09143) and a second round of PCR using Clontech primer AP2
CC (AAA09148) and a gene-specific primer 2 (AAA09144-47). Clones were
CC sequenced for verification and then amplified with Clontech primer AP3
CC (AAA09148) and a gene-specific primer (AAA09149-52). The promoters are
CC used for regulating the expression of heterologous nucleotide sequences
CC to vary the phenotype of a plant, e.g. modifying fatty acid composition,
CC altering amino acid content and altering the pathogen defense system of
CC the plant. Plants comprising important commercial traits can be
CC generated.

SO Sequence 32 BP; 8 A; 12 C; 6 G; 6 T; 0 other;

Query Match 77.1%; Score 16.2; DB 21; Length 32;

Best Local Similarity 85.7%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
|||||
3 CAGCAGCAGAGCTTCATCAT 23

SULT 4
A11024/c
AAA11024 standard; DNA; 50 BP.

AAA11024;

28-UTL-2000 (first entry)

Human mature Interleukin 18 binding protein coding sequence primer #2.

Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
regulator; drug; sensitivity disease; organ rejection; organ transplant;
autoimmune disease; PCR primer; ss.

Homo sapiens.

MO200012555-A1.

09-MAR-2000.

18-NOV-1998; 98WO-JP05186.

01-SEP-1998; 98JP-0247588.

18-NOV-1998; 98JP-0327914.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Torigoe K, Tanai M, Kurimoto M;

WPI 2000-237850/20.

Interleukin 18-binding protein with activity of regulating
physiological actions of interleukin 18, useful as regulator and drug
for sensitivity disease and organ rejection and in treating diseases
due to excess immune reaction

Example 2; Page 22; 71pp; Japanese.

The invention relates to novel interleukin 18 (IL-18)-binding proteins
from humans or mice which act as regulators and drugs for sensitivity
diseases and organ rejection and in treating diseases due to excess
immune reaction, e.g. in slowing down rejection after organ transplant,
and in treating autoimmune diseases. This sequence represents a PCR
primer used to isolate the coding sequence for the human mature
interleukin 12 binding protein (AAA11002).

Sequence 50 BP; 7 A; 11 C; 18 G; 14 T; 0 other;

Query Match 77.1%; Score 16.2; DB 21; Length 50;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCATCAT 21
|||||
44 CAGCAGCAGAGCTTCATCAT 24

UTL 5

15291

AA15291 standard; DNA; 22 BP.

AA15291;

16-JAN-2002 (first entry)

DB Mouse IL-12 p40 #1 PCR primer 662F.

KW Mouse; ss; PCR primer; neuroprotective; 662F;
KW antiinflammatory; interleukin-1beta; IL-1b; tumour necrosis factoralpha;
KW TNFalpha; macrophage inflammatory protein-1alpha; MIP-1alpha;
KW fractalkine; glial fibrillar associated protein; GFAP; MHC; CX3CR1; CD86;
KW major histocompatibility complex; Alzheimer's disease; cerebral ischaemia;
KW neurodegenerative disease; Vldl-24OHase; MCP-1; IL-10; IL-12 p40;
KW IFN-gamma; CD3 epsilon; CD4; IgG-1; Ig k; osteopontin.

Mus sp.

MO200175165-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10247.

30-MAR-2000; 2000US-193847P.

(ELAN) ELAN PHARM INC.

McConlogue LC, Games KD, Yednock TA, Hua T, Messersmith E, Bard F;

WPI; 2001-639367/73.

Selecting compounds useful for treating or preventing Alzheimer's
disease, from their ability to reduce levels of specific disease
markers in animal models

Example 5; Page 23; 36pp; English.

The invention relates selecting compounds that reduce symptoms of
Alzheimer's disease using a non-human mammal that has been subjected to
cerebral ischaemia or lesion of a nerve so as to produce, in the
affected region, increased levels of specific markers of Alzheimer's
disease-associated inflammation. Test compounds are selected if they
reduce levels of these markers significantly, in the affected region,
relative to controls. The markers are interleukin-1beta (IL-1b), tumour
necrosis factoralpha (TNFalpha), macrophage inflammatory protein-1alpha
(MIP-1alpha), glial fibrillar associated protein (GFAP), MHC (major
histocompatibility complex) Iialpha or II L, CD86, fractalkine or CX3CR1
(a receptor for fractalkine). The method is used to identify compounds
useful in treatment or prevention of Alzheimer's disease or other
neurodegenerative diseases that have an inflammatory component. The
method provides fast, accurate and quantitative drug screens. The
present sequence is a PCR primer used to determine the level of
a transcript for an efficacy marker in a transgenic mouse which
overexpresses APP and displays Alzheimer's like neuropathy. The
efficacy markers are Vldl-24OHase, MCP-1, IL-10, IL-12 p40, #1/#2,
IFN-gamma #1/#2, CD3 epsilon, CD4 #1/#2, IgG-1, Ig k (light chain).

Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 other;

Query Match 72.4%; Score 15.2; DB 22; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0y 1 CAGCAGCAGAGCTTCATCA 20
|||||
Db 2 CAGCAGCAGAGCTTCATCA 21

RESULT 6

AA296146/c

ID AA296146 standard; DNA; 40 BP.

AA296146;

10-APR-2000 (first entry)

Polynucleotide sequence including binding site for BamHI.

Ligand binding; restriction enzyme; nucleic acid determination; pharmaceutical; BamHI; ss.

Synthetic.

WO9963077-A2.

09-DEC-1999.

04-JUN-1999; 99MO-US12516.

04-JUN-1998; 98US-0087905.

03-JUN-1999; 99US-0324672.

(TMTR-) TM TECHNOLOGIES INC.

Lane MJ, Benight AS, Faldasz BD;

WPI, 2000-116369/10.

Modulating polynucleotide ligand binding site affinity using determination of the flanking duplex sequences -

Example 1; Page 45; 62pp; English.

The invention provides a method for determining the sequence of polynucleotide flanking regions that modulate ligand binding characteristics of an adjacent binding site. The method comprises: (i) providing a number of different duplex polynucleotides, each having the same polynucleotide ligand binding site and a randomly synthesized sequence flanking the binding site; (ii) exposing the duplex to a ligand selective for the binding site; (iii) isolating duplexes which bind or do not bind the ligand, and (iv) determining the nucleotide composition of the flanking duplex sequence by sequencing the duplex sequence adjacent to the binding site. The invention is used to modulate the ligand-binding characteristics of any nucleotide sequence. The invention is less costly and more efficient than prior art techniques that moderate ligand binding using small molecule pharmaceuticals. Sequences AA295762-296170 represent polynucleotide sequences including the binding site for the restriction enzyme BamHI and used in the course of the invention.

Sequence 40 BP; 6 A; 5 C; 19 G; 10 T; 0 other;

Very Match 72.4%; Score 15.2; DB 21; Length 40; Best Local Similarity 85.0%; Pred. No. 1.7e+03; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGAGGCTTCATCA 20
|||||
28 CAGCAGACGCTCTCTCA 9

FLT 7

30863/C
ABQ80863 standard; DNA; 33 BP.

ABQ80863;

18-DEC-2002 (first entry)

Hexapetoloid duplication inclusion transference 14.96 PCR primer #3.

Hexapetoloid duplication inclusion transference 14.96; transference; enzyme; tumour; haemopathy; HIV infection; immunological disease; inflammation; cytostatic; anti-HIV; anti-inflammatory; PCR; primer; ss.

Unidentified.

CN1352267-A.

05-JUN-2002.

PF 02-NOV-2000; 2000CN-0127170.
XX
PR 02-NOV-2000; 2000CN-0127170.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI, 2002-628715/68.
XX
PT New hexapetoloid duplication inclusion transference 14.96 polypeptide for
PT treating malignant tumours, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations -
XX
PS Example 4; Page 18 (disclosure); 33pp; Chinese.
XX
CC The present invention relates to hexapetoloid duplication inclusion
CC transference 14.96 (see ABQ80860 and ABQ80863). The transference and its
CC coding sequence are useful for treating various diseases, such as
CC malignant tumours, haemopathy, HIV infection, immunological diseases
CC and various inflammations. The present sequence is a PCR primer, which
CC was used in an example from the invention.
XX
SQ Sequence 33 BP; 10 A; 8 C; 7 G; 8 T; 0 other;
XX
Query Match 71.4%; Score 15; DB 24; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 7 CAGAGCTTCATCAT 21
Db 21 CAGAGCTTCATCAT 7
RESULT 8
AAA94223
ID AAA94223 standard; DNA; 21 BP.
XX
AC AAA94223;
XX
DT 12-JUN-2001 (first entry)
XX
DE Murine testosterone-repressed prostate message-2 antisense oligo #1.
XX
KM Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KM sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS hns sp.
XX
FH Key Location/Qualifiers
FH modified_base 1 /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000MO-US04875.
XX
PR 26-FEB-1999; 99US-0121726.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX
DR WPI, 2000-533132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene -
XX
PS Example 1; Page 35; 38pp; English.

2 AGCAGCAGCTTCATCA 20
|||||
22 AGCAGCAGCTTCATCA 4

ULF 11
12445/C
AAZ12445 standard; DNA; 30 BP.

AAZ12445;

08-OCT-1999 (first entry)

PCR primer used to amplify ORF3 of *Neisseria* species.

Neisseria meningitidis; *Neisseria gonorrhoeae*; antigen; vaccine;
treatment; *Neisseria* infection; meningitis; septicemia; gonorrhea;
PCR primer; 88.

Synthetic.
Neisseria sp.

MO9924578-A2.

20-MAY-1999.

09-OCT-1998; 98WO-IB01665.

01-SEP-1998; 98GB-0019016.
06-NOV-1997; 97GB-0023516.
14-NOV-1997; 97GB-0024190.
18-NOV-1997; 97GB-0024386.
27-NOV-1997; 97GB-0025158.
10-DEC-1997; 97GB-0026147.
14-JAN-1998; 98GB-0000759.

(CHIR-) CHIRON SPA.

Grandi G, Maignani V, Piazza M, Rappuoli R, Scarlato V;

WPI; 1999-327407/27.

Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for
diagnosis, treatment and prevention of infection.

Disclosure; Page 489; 524p; English.

PCR primers AAZ12359-212531 were used to amplify various open reading
frames (ORFs) of *Neisseria meningitidis* and *N. gonorrhoeae*. These
ORFs (AAZ11972-212358) encode antigenic proteins (AAJ38499-Y38944). The
antigenic proteins, their fragments, their nucleic acids and antibodies
are used for diagnosis, prevention (as vaccines) or treatment of
Neisseria infections, such as meningitis, septicemia and gonorrhea.
Both organisms are closely related. Fragments of the nucleic acids are
useful as hybridisation probes and antisense reagents.

Sequence 30 BP; 7 A; 10 C; 7 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 30;
Best Local Similarity 88.9%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGCTTCAT 18
|||||
29 CAGCAGCAGCTTCAT 12

LT 12

9972/C
AA069972 standard; cDNA; 31 BP.

AA069972;

XX 25-MAR-2003 (updated)
DT 13-MAR-1995 (first entry)
XX

5'sense leader ex oligo primer to amplify 5' end Can fi cDNA.

XX Canis familiaris; protein allergen; dog dander; dog hair; allergy;
XX T cell response; stimulation; diagnosis; sensitivity; therapeutic;
XX agents; PCR; polymerase chain reaction; primer; amplification;
XX probe; hybridisation; partial cDNA; degenerate; 88.

XX Synthetic.

XX MO9416068-A2.

XX 21-JUL-1994.

XX 30-DEC-1993; 93WO-US12468.

XX 31-DEC-1992; 92US-0999712.

XX 22-NOV-1993; 93US-0156549.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Bizenkauskas CB, Brauer AW, Konieczny A, Morgenstern JP;

XX WPI; 1994-249215/30.

XX DNA encoding dog dander allergenic peptide(s) Can f I and Can f

XX IT - used in the diagnosis and treatment of sensitivity to dog

XX dander

XX Example 2; Page 59; 124p; English.

XX AA069972 is a 5' primer corresponding to residues -26 to -20 of Canfi
XX (AAK5987). It is used with AA069973 to amplify and sequence the 5'end
XX of the Can fi cDNA. Peptides of the invention have the ability to
XX induce a T cell response, which may include T cell stimulation or
XX T cell nonresponsiveness. Some have the ability to bind the dog
XX dander specific IgE of dog dander allergic subjects. These peptides
XX are useful in diagnosing sensitivity to dog dander. Other peptides
XX significantly reduce the ability to bind dog dander allergic IgE and
XX are thus useful as therapeutic agents. (See also AA069951-070006 and
XX AAK5987-60018 - these include primers, and probes for isolation of
XX cDNA coding Can fi and fii allergens and peptides derived from the
XX sequences.)
XX (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 31 BP; 7 A; 13 C; 5 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 15; Length 31;

Best Local Similarity 88.9%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AGCAGCAGCTTCATC 19
|||||
Db 24 AGCAGCAGCTTCATC 7

RESULT 13
ABL61345/C

ID ABL61345 standard; DNA; 24 BP.

XX ABL61345;

XX 13-SEP-2002 (first entry)

XX Najia najia atra short chain neurotoxin-associated PCR primer #1.

XX Chinese cobra; neurotoxin; cancer; PCR; primer; 88.

XX Najia najia atra.

PN CN1337404-A.
 XX 27-FEB-2002.
 XX 03-AUG-2000; 2000CN-0119561.
 XX 03-AUG-2000; 2000CN-0119561.
 XX 03-AUG-2000; 2000CN-0119561.
 XX (SHAN-) SHANGHAI BIOENGINEERING RES CENT CHINESE.
 XX Cai Q, Yang S, Gong Y;
 XX WPI; 2002-384228/42.
 XX Short-chain nervous cobra toxin, its preparation and use -
 XX Example 1; Page 11; 30pp; Chinese.
 XX This invention describes a novel cobra short chain neurotoxin, the
 XX polynucleotide encoding the polypeptide and the method for producing the
 XX polypeptide by means of recombination technology. The invention also
 XX discloses the method for curing several diseases, such as cancer, by
 XX using the cobra short chain neurotoxin, and a medicine composite
 XX containing the cobra short chain neurotoxin. This sequence represents a
 XX PCR primer used in the amplification of the short chain neurotoxin
 XX described in the method of the invention.
 XX Sequence 24 BP; 7 A; 5 C; 6 G; 6 T; 0 other;
 XX
 XX Query Match 69.5%; Score 14.6; DB 24; Length 24;
 XX Best Local Similarity 81.0%; Pred. No. 3e+03;
 XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 XX 1 CAGCAGCAGAGCTTCATCAT 21
 XX 21 CAGCAGCAGAGCTTCATCTT 1
 XX
 XX RESULT 14
 XX BK49118/c
 XX D ABK49118 standard; DNA; 33 BP.
 XX C ABK49118;
 XX 02-JUL-2002 (first entry)
 XX Human transcription factor LCR-F19.02 PCR primer #1.
 XX Human; ss; transcription factor; LCR-F19.02; erythropoathy; PCR; primer.
 XX Homo sapiens.
 XX MO20020583-A1.
 XX 14-MAR-2002.
 XX 25-JUN-2001; 2001MO-CN01053.
 XX 28-JUN-2000; 2000CN-0116822.
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX Mao Y, Xie X;
 XX WPI; 2002-351761/38.
 XX Homo transcription factor F19.02 and encoding polynucleotide, used in
 XX treatment of erythropoathy -
 XX Example 4; Page 18; 38pp; Chinese.
 XX The invention relates to an isolated polypeptide of human (HOMO)
 XX transcription factor LCR-F19.02 the cDNA encoding it, and its fragment,

CC analogue or derivative. Also included are vectors expressing the protein,
 CC a host cell comprising the vector, the isolation of modulators of the
 CC protein and an anti-transcription factor LCR-F19.02 antibody. The protein
 CC and nucleic acid are used in diagnosis and treatment of erythropoathy.
 CC The present sequence is a PCR primer used to clone the cDNA encoding
 CC transcription factor LCR-F19.02.
 CC
 CC Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 other;
 CC
 CC Query Match 69.5%; Score 14.6; DB 24; Length 33;
 CC Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 CC Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC 1 CAGCAGCAGAGCTTCATCAT 21
 CC 27 CAGCAGCAGAGCTTCATCAT 7
 CC
 CC RESULT 15
 CC ID AAH79384/c
 CC AAH79384 standard; DNA; 34 BP.
 CC AC AAH79384;
 CC 04-DEC-2001 (first entry)
 CC DE Plasmolemma regulation function-contained protein 70 cDNA PCR primer #3.
 CC KM Plasmolemma regulation function-contained protein 70; cancer; HIV;
 CC KM infection; gene therapy; human; PCR primer; ss.
 CC OS Homo sapiens.
 CC XX CN1302889-A.
 CC 11-JUL-2001.
 CC 29-OCT-1999; 99CN-0119927.
 CC XX 29-OCT-1999; 99CN-0119927.
 CC PR 29-OCT-1999; 99CN-0119927.
 CC PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
 CC PI Mao Y, Xie Y;
 CC WPI; 2001-566050/64.
 CC PT Polypeptide-human protein 70 containing plasmolemma regulation function
 CC and polynucleotide for coding it -
 CC Example 5; Page 15(Disclosure); 27pp; Chinese.
 CC The present invention provides the protein and coding sequences of human
 CC plasmolemma regulation function-contained protein 70. The sequences can
 CC be used in the treatment of cancer and HIV infection. The present
 CC sequence is a PCR primer for the coding sequence of the invention.
 CC
 CC Sequence 34 BP; 5 A; 9 C; 9 G; 11 T; 0 other;
 CC
 CC Query Match 69.5%; Score 14.6; DB 22; Length 34;
 CC Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 CC Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC 1 CAGCAGCAGAGCTTCATCAT 21
 CC 27 CAGCAGCAGAGCTTCATCAT 7
 CC

Search completed: November 8, 2003, 02:53:16
 Job time : 252 secs

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nucleic - nucleic search, using sw model

on: November 8, 2003, 02:44:45 ; Search time 69 Seconds
(without alignments)

134.334 Million cell updates/sec

file: US-09-944-326-4

reference score: 1 cagcagcagagctctcatcat 21

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total number of hits satisfying chosen parameters: 744296

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

abase: Issued Patents NA:*

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4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

5: /cgn2_6/prodata/2/ina/5A_COMB.seq:*

6: /cgn2_6/prodata/2/ina/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	16.2	77.1	32	4	US-09-410-935B-6
2	15.4	73.3	45	1	US-07-885-689A-7
3	14.8	70.5	31	2	US-08-467-603-35
4	14.8	70.5	31	2	US-08-467-603-35
5	14.8	70.5	31	2	US-08-467-603-35
6	14.8	70.5	31	2	US-08-467-603-35
7	14.6	69.5	44	3	US-09-374-671A-35
8	14.2	67.6	20	4	US-09-110-959A-11
9	14.2	67.6	20	4	US-09-205-860-3
10	14.2	67.6	24	4	US-09-657-452A-163
11	14.2	67.6	30	3	US-09-360-545-57
12	14.2	67.6	30	3	US-09-130-663-10
13	14.2	67.6	30	3	US-09-432-335-10
14	14.2	67.6	30	3	US-09-254-023B-20
15	14.2	67.6	30	4	US-09-614-022-10
16	13.8	65.7	18	4	US-09-422-978-3015
17	13.8	65.7	37	2	US-08-467-603-35
18	13.8	65.7	37	2	US-08-467-603-35
19	13.8	65.7	37	2	US-08-467-603-35
20	13.8	65.7	37	2	US-08-467-603-35
21	13.6	64.8	20	4	US-09-374-671A-35
22	13.6	64.8	20	4	US-09-517-467B-87
23	13.6	64.8	23	4	US-09-198-452A-4550
24	13.6	64.8	27	6	5463174-1
25	13.6	64.8	50	4	US-09-996-243-312
26	13.4	63.8	20	4	US-09-657-452A-162
27	13.4	63.8	34	1	US-08-373-124A-27

c	28	13.4	63.8	34	1	US-08-435-628-27	Sequence 27, Appl
c	29	13.2	62.9	18	2	US-09-205-860-28	Sequence 28, Appl
c	30	13.2	62.9	24	4	US-09-442-099A-9	Sequence 9, Appl
c	31	13.2	62.9	24	4	US-09-612-342-9	Sequence 9, Appl
c	32	13.2	62.9	33	2	US-08-343-443B-100	Sequence 100, Appl
c	33	13.2	62.9	38	3	US-09-130-663-26	Sequence 26, Appl
c	34	13.2	62.9	38	3	US-09-432-978-7130	Sequence 26, Appl
c	35	13.2	62.9	38	4	US-09-614-022-26	Sequence 26, Appl
c	36	13.2	62.9	47	4	US-09-422-978-7130	Sequence 26, Appl
c	37	13.2	62.9	19	4	US-08-390-850-93	Sequence 26, Appl
c	38	13.2	62.9	23	1	US-08-390-850-93	Sequence 26, Appl
c	39	13.2	62.9	23	1	US-08-390-850-93	Sequence 26, Appl
c	40	13.2	62.9	31	1	US-08-390-850-93	Sequence 26, Appl
c	41	13.2	62.9	31	1	US-08-390-850-93	Sequence 26, Appl
c	42	13.2	62.9	31	1	US-08-390-850-93	Sequence 26, Appl
c	43	13.2	62.9	31	1	US-08-390-850-93	Sequence 26, Appl
c	44	13.2	62.9	31	1	US-08-390-850-93	Sequence 26, Appl
c	45	13.2	62.9	31	1	US-08-390-850-93	Sequence 26, Appl

ALIGNMENTS

```

RESULT 1
US-09-410-935B-6
; Sequence 6, Application US/09410935B
; Patent No. 6504083
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Enclaire Meyer, Terry
; APPLICANT: Rtd Saad, Mohammed
; TITLE OR INVENTION: No. 6504083el Maize Promoters
; FILE REFERENCE: 5718-72
; CURRENT APPLICATION NUMBER: US/09/410,935B
; CURRENT FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 60/103,294
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 1 for Gps-2
US-09-410-935B-6

Query Match
Best Local Similarity 77.1%; Score 16.2; DB 4; Length 32;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CAGCAGCAGAGCTCTCATCAT 21
Db 3 CAGCAGCAGAGCTCTCATCAT 23

RESULT 2
US-07-885-689A-7
; Sequence 7, Application US/07885689A
; Patent No. 536876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OR INVENTION: Method for Production of Bovine Growth
; HORMONE Using a Synthetic Gene.
; NUMBER OF SEQUENCES: 38

```

CORRESPONDENCE ADDRESS:
 ADDRESSER: Birch, Stewart, Kolash & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/885,689A
 FILING DATE: 19-MAY-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Svensson, Leonard R.
 REGISTRATION NUMBER: 30,330
 REFERENCE/DOCKET NUMBER: 377-144P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-241-1300
 TELEFAX: 703-241-2848

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYPOTHEICAL: NO
 FEATURE:

NAME/KEY: 1.45
 LOCATION: 1.45
 OTHER INFORMATION: /label= oligonucleotide
 OTHER INFORMATION: /note= "U7 oligonucleotide portion of synthetic
 OTHER INFORMATION: Bgh gene, Figure 1."

17-885-689A-7

Very Match 73.3%; Score 15.4; DB 1; Length 45;
 Percent Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 CAGCAGAGTCTTCATCA 20
 |||||
 21 CAGCAGAGTCTTCACCA 37

LT 3
 8-467-603-35/c
 Sequence 35, Application US/08467603
 Patent No. 5843672

GENERAL INFORMATION:
 APPLICANT: Morgenstern, Jay P.
 APPLICANT: Kamieczny, Andrzej
 APPLICANT: Bizindaukas, Christine B.
 APPLICANT: Brauer, Andrew W.
 TITLE OF INVENTION: Allergenic Proteins and
 TITLE OF INVENTION: Peptides from Dog
 TITLE OF INVENTION: Dander and Uses Therefor
 NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
 ADDRESSER: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII-text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,603
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/156,549
 FILING DATE:
 APPLICATION NUMBER: 07/999,712
 FILING DATE: 31-Dec-92
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

US-08-467-603-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;
 Percent Local Similarity 88.9%; Pred. No. 4.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19
 |||||
 Db 24 AGCAGCAGAGTCTTCATC 7

RESULT 4
 US-08-466-793-35/c
 Sequence 35, Application US/08466793
 Patent No. 5891716

GENERAL INFORMATION:
 APPLICANT: Morgenstern, Jay P.
 APPLICANT: Kamieczny, Andrzej
 APPLICANT: Bizindaukas, Christine B.
 APPLICANT: Brauer, Andrew W.
 TITLE OF INVENTION: Allergenic Proteins and
 TITLE OF INVENTION: Peptides from Dog
 TITLE OF INVENTION: Dander and Uses Therefor
 NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
 ADDRESSER: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII-text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,793
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/156,549
 FILING DATE: 22-NOV-1993
 APPLICATION NUMBER: 07/999,712
 FILING DATE: 31-Dec-92

ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
-08-466-793-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;
Best Local Similarity 88.9%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2 AGCAGCAGGCTTCATC 19
|||
24 AGCAGCAGGCTTCATC 7

SUPT 5
-08-491-861A-35/c
Sequence 35, Application US/08491861A
Patent No. 5939283
GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.
APPLICANT: Kaniecny, Andrzej
APPLICANT: Bizindauskas, Christine B.
APPLICANT: Brainer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESSES:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,861A
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:

NAME: Mandragoras, Amy B.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
-08-491-861A-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;
Best Local Similarity 88.9%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2 AGCAGCAGGCTTCATC 19
|||
24 AGCAGCAGGCTTCATC 7

Db 24 AGCAGCAGGCTTCATC 7

RESULT 6
US-09-374-671A-35/c
Sequence 35, Application US/09374671A
Patent No. 6489118
GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.
APPLICANT: Kaniecny, Andrzej
APPLICANT: Bizindauskas, Christine B.
APPLICANT: Brainer, Andrew W.
TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSER: Amy B. Mandragoras
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671A
FILING DATE: 16-Aug-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,549
FILING DATE: 1993-NOV-22
APPLICATION NUMBER: US 07/999,712
FILING DATE: 1992-DEC-31
ATTORNEY/AGENT INFORMATION:

NAME: DiGiorgio, Jeanne M.
REGISTRATION NUMBER: 41,710
REFERENCE/DOCKET NUMBER: IMI-026C2CNCRA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-374-671A-35

Query Match

Best Local Similarity 70.5%; Score 14.8; DB 4; Length 31;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGCAGCAGGCTTCATC 19
|||
24 AGCAGCAGGCTTCATC 7

US-09-110-959A-11
Sequence 11, Application US/09110959A
Patent No. 6268197
GENERAL INFORMATION:

APPLICANT: Schulteis, Martin
APPLICANT: Outtrup, Helie
APPLICANT: Jorgensen, Per Lina
APPLICANT: Bjornvad, Mads Skelund
TITLE OF INVENTION: Alkaline Xyloglucanase
FILE REFERENCE: 5206.200-US
CURRENT APPLICATION NUMBER: US/09/110,959A

CURRENT FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 0822/97
 PRIOR FILING DATE: 1997-07-07
 PRIOR APPLICATION NUMBER: 1213/97
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/054,039
 PRIOR FILING DATE: 1997-07-28
 PRIOR APPLICATION NUMBER: 60/063,694
 PRIOR FILING DATE: 1997-10-28
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 44
 TYPE: DNA
 ORGANISM: Bacillus sp.
 19-110-959A-11

Very Match 69.5%; Score 14.6; DB 3; Length 44;
 Best Local Similarity 81.0%; Pred. No. 5.6e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATC 21
 12 CAGCAGCAGCAGGCTTCATC 32

LT 8
 19-205-860-3
 Sequence 3, Application US/09205860
 Patent No. 5981732
 INVENTOR: Lex M. Cowart
 APPLICANT: Lex M. Cowart
 TITLE OF INVENTION: ANTISENSE MODULATION OF 6-ALPHA-13 EXPRESSION
 FILE REFERENCE: RTS-0031
 CURRENT APPLICATION NUMBER: US/09/205,860
 CURRENT FILING DATE: 1998-12-04
 NUMBER OF SEQ ID NOS: 87
 SEQ ID NO 3
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: PCR Primer
 19-205-860-3

Very Match 67.6%; Score 14.2; DB 2; Length 20;
 Best Local Similarity 84.2%; Pred. No. 7.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATC 19
 2 CAGCAGCAGAGTCTTCAC 20

LT 9
 19-657-452A-163
 Sequence 163, Application US/09657452A
 Patent No. 6426188
 INVENTOR: Jacqueline Wyatt
 APPLICANT: Brecht P. Monla
 TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 1 EXPRESSION
 FILE REFERENCE: RTS-0125
 CURRENT APPLICATION NUMBER: US/09/657,452A
 CURRENT FILING DATE: 2000-09-07
 NUMBER OF SEQ ID NOS: 178
 SEQ ID NO 163
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
 19-657-452A-163

Query Match 67.6%; Score 14.2; DB 4; Length 20;
 Best Local Similarity 84.2%; Pred. No. 7.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
 DB 2 CATCATCATATGCTTCATC 20

RESULT 10
 US-09-360-545-57/c
 Sequence 57, Application US/09360545
 Patent No. 6429014
 GENERAL INFORMATION:
 APPLICANT: Croteau, Rodney B
 APPLICANT: Bohlmann, Jorg
 APPLICANT: Steele, Christopher L
 APPLICANT: Phillips, Michael A
 TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 FILE REFERENCE: wau-13885
 CURRENT APPLICATION NUMBER: US/09/360,545
 CURRENT FILING DATE: 1999-07-26
 EARLIER APPLICATION NUMBER: 60/052,249
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: PCT/US98/14528
 EARLIER FILING DATE: 1998-07-10
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 57
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: oligonucleotide corresponding to amino acid
 OTHER INFORMATION: sequence set forth in SEQ ID NO:46
 NAME/KEY: misc feature
 LOCATION: (1)..(24)
 OTHER INFORMATION: oligonucleotide that corresponds to the conserved
 OTHER INFORMATION: amino acid sequence set forth in SEQ ID NO:46
 US-09-360-545-57

Query Match 67.6%; Score 14.2; DB 4; Length 24;
 Best Local Similarity 84.2%; Pred. No. 7.6e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
 DB 24 CAGCAGCAGAGTCTTCAC 6

RESULT 11
 US-09-130-663-10/c
 Sequence 10, Application US/09130663A
 Patent No. 6020163
 GENERAL INFORMATION:
 APPLICANT: Conklin, Darrell C.
 TITLE OF INVENTION: LIPOCALIN HOMOLOG
 FILE REFERENCE: 97-24
 CURRENT APPLICATION NUMBER: US/09/130,663A
 CURRENT FILING DATE: 1998-08-05
 EARLIER APPLICATION NUMBER: 60/054,867
 EARLIER FILING DATE: 1997-08-06
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 10
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Oligonucleotide primer: ZC13270
 19-657-452A-163


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RESULT 15
US-09-422-978-3015/C
; Sequence 3015, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET .020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850

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EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 3015
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-21687-313 : polymorphic base G or A
99-422-978-3015
Very Match 67.6%; Score 14.2; DB 4; Length 47;
Percent Local Similarity 76.2%; Pred. No. 8.5e+02;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
1 CAGCAGCAGAGCTTCATCAT 21
35 CAGATCAGCAGCTTCATCTT 15
Job completed: November 8, 2003, 03:51:37
Time : 70 secs

GenCore version 5.1.6
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1 nucleic - nucleic search, using sw model

on on: November 8, 2003, 03:17:20 ; Search time 240 Seconds
(without alignments)

279.209 Million cell updates/sec

file: US-09-944-326-4

reference: 1 cagcagcagagcttcctcatcat 21

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Gapop 10.0, Gapext 1.0

arched: 2141354 seqs, 1595478879 residues

cal number of hits satisfying chosen parameters: 1180526

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st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	length	DB ID	Description
1	21	100.0	21	10	US-09-944-326-4
2	21	100.0	21	12	US-09-967-726A-4
3	21	100.0	21	12	US-10-080-794-4
4	17.8	84.8	21	12	US-09-967-726A-15
5	17.8	84.8	21	12	US-10-080-794-15
6	16.2	77.1	32	14	US-10-278-255-6
7	14.8	70.5	20	14	US-10-007-010-43
8	14.8	70.5	21	10	US-09-944-326-1
9	14.8	70.5	21	10	US-09-944-326-2
10	14.8	70.5	21	12	US-09-967-726A-1
11	14.8	70.5	21	12	US-09-967-726A-2
12	14.8	70.5	21	12	US-10-080-794-1
13	14.8	70.5	21	12	US-10-080-794-2
14	14.8	70.5	31	9	US-09-374-671-35
15	14.8	70.5	31	14	US-10-196-107A-35
16	14.2	67.6	22	11	US-09-946-374-163

C 17	14.2	67.6	22	12	US-10-015-387A-163	Sequence 163, App
C 18	14.2	67.6	22	12	US-10-006-130A-163	Sequence 163, App
C 19	14.2	67.6	22	12	US-10-006-172A-163	Sequence 163, App
C 20	14.2	67.6	22	12	US-10-015-392A-163	Sequence 163, App
C 21	14.2	67.6	22	12	US-10-017-253A-163	Sequence 163, App
C 22	14.2	67.6	22	12	US-10-017-306A-163	Sequence 163, App
C 23	14.2	67.6	22	12	US-10-012-064A-163	Sequence 163, App
C 24	14.2	67.6	22	12	US-10-017-867A-163	Sequence 163, App
C 25	14.2	67.6	22	12	US-10-012-101B-163	Sequence 163, App
C 26	14.2	67.6	22	12	US-10-012-137A-163	Sequence 163, App
C 27	14.2	67.6	22	12	US-10-012-752A-163	Sequence 163, App
C 28	14.2	67.6	22	12	US-10-012-752A-163	Sequence 163, App
C 29	14.2	67.6	22	12	US-10-013-909A-163	Sequence 163, App
C 30	14.2	67.6	22	12	US-10-013-910A-163	Sequence 163, App
C 31	14.2	67.6	22	12	US-10-013-911A-163	Sequence 163, App
C 32	14.2	67.6	22	12	US-10-013-912A-163	Sequence 163, App
C 33	14.2	67.6	22	12	US-10-015-610A-163	Sequence 163, App
C 34	14.2	67.6	22	12	US-10-015-653A-163	Sequence 163, App
C 35	14.2	67.6	22	12	US-10-015-671A-163	Sequence 163, App
C 36	14.2	67.6	22	12	US-10-012-237A-163	Sequence 163, App
C 37	14.2	67.6	22	12	US-10-013-906A-163	Sequence 163, App
C 38	14.2	67.6	22	12	US-10-015-388A-163	Sequence 163, App
C 39	14.2	67.6	22	12	US-10-015-480A-163	Sequence 163, App
C 40	14.2	67.6	22	12	US-10-015-715A-163	Sequence 163, App
C 41	14.2	67.6	22	12	US-10-012-753A-163	Sequence 163, App
C 42	14.2	67.6	22	12	US-10-015-385A-163	Sequence 163, App
C 43	14.2	67.6	22	12	US-10-007-236A-163	Sequence 163, App
C 44	14.2	67.6	22	12	US-10-015-389A-163	Sequence 163, App
C 45	14.2	67.6	22	12	US-10-013-915A-163	Sequence 163, App

ALIGNMENTS

RESULT 1
US-09-944-326-4
Sequence 4, Application US/09944326
Patent No. US20020128220A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Remite, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
FILE REFERENCE: UBC-P-020-2
CURRENT APPLICATION NUMBER: US/09/944,326
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 21
TYPE: DNA
ORGANISM: HUMAN
FEATURES:
OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4
Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTTCATCAT 21
DB 1 CAGCAGCAGAGCTTCATCAT 21
RESULT 2
US-09-967-726A-4
Sequence 4, Application US/09967726A

APPLICANT: Barbour, Eric
APPLICANT: Bucalire Meyer, Terry
APPLICANT: Bid Saad, Mohammed
TITLE OF INVENTION: No. US20030097690A1el Maize Promoters
FILE REFERENCE: 5718-72
CURRENT APPLICATION NUMBER: US/10/278,255
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: US/09/410,935
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 60/107,201
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 60/103,294
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Gene specific primer 1 for Gcs-2
3-10-278-255-6

Query Match 77.1%; Score 16.2; DB 14; Length 32;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
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3 CAGCAGCAGAGTCTTCATCAT 23

RESULT 7
-10-007-010-43
Sequence 43, Application US/10007010
Publication No. US2003012275A1
GENERAL INFORMATION:
APPLICANT: Alexander H. Borchers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
FILE REFERENCE: RTS-0345
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 43
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
-10-007-010-43

Query Match 70.5%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GCAGCAGAGTCTTCATCA 20
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1 GCAGCAGAGTCTTCATCA 18

SULT 8
-09-944-326-1
Sequence 1, Application US/09944326
Patent No. US20020128220A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
FILE REFERENCE: UBC.P-020-2
CURRENT APPLICATION NUMBER: US/09/944,326

CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-1

Query Match 70.5%; Score 14.8; DB 10; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCAT 18
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4 CAGCAGCAGAGTCTTCAT 21

RESULT 9
US-09-944-326-2
Sequence 2, Application US/09944326
Patent No. US20020128220A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
FILE REFERENCE: UBC.P-020-2
CURRENT APPLICATION NUMBER: US/09/944,326
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 21
TYPE: DNA
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: mismatch control
US-09-944-326-2

Query Match 70.5%; Score 14.8; DB 10; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCAT 18
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4 CAGCAGCAGAGTCTTCAT 21

RESULT 10
US-09-967-726A-1
Sequence 1, Application US/0996726A
Publication No. US20030158130A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
APPLICANT: Zellweger, Tobias
TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
FILE REFERENCE: UBC.P-022

CURRENT APPLICATION NUMBER: US/09/967,726A
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
ORGANISM: human
-09-967-726A-1

Query Match 70.5%; Score 14.8; DB 12; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 18
|||||
4 CAGCAGCAGAGCTTCAT 21

ULT 11
-09-967-726A-2
Sequence 2, Application US/09967726A
Publication No. US2003015810A1
GENERAL INFORMATION:

APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
APPLICANT: Zellweger, Tobias
TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: UBC-P-022
CURRENT APPLICATION NUMBER: US/09/967,726A
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2

LENGTH: 21
TYPE: DNA
ORGANISM: human
-09-967-726A-2

Query Match 70.5%; Score 14.8; DB 12; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCAGCAGAGCTTCAT 18
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4 CAGCAGCAGAGCTTCAT 21

ULT 12
-10-080-794-1
Sequence 1, Application US/10080794
Publication No. US2003016591A1
GENERAL INFORMATION:

APPLICANT: Rennie, Martin
APPLICANT: Gleave, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
FILE REFERENCE: UBC-P-020-3
CURRENT APPLICATION NUMBER: US/10/080,794
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 09/944,326
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-1

Query Match 70.5%; Score 14.8; DB 12; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCAT 18
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Db 4 CAGCAGCAGAGCTTCAT 21

RESULT 13

US-10-080-794-2
Sequence 2, Application US/10080794
Publication No. US2003016591A1
GENERAL INFORMATION:

APPLICANT: Gleave, Martin
APPLICANT: Rennie, Paul S.
APPLICANT: Miyake, Hideaki
APPLICANT: Nelson, Colleen
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
FILE REFERENCE: UBC-P-020-3
CURRENT APPLICATION NUMBER: US/10/080,794
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/121,726
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/913,325
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 09/944,326
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

LENGTH: 21
TYPE: DNA
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: mismatch control
US-10-080-794-2

Query Match 70.5%; Score 14.8; DB 12; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCAT 18
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Db 4 CAGCAGCAGAGCTTCAT 21

RESULT 14

US-09-374-671-35/c
Sequence 35, Application US/09374671
Patent No. US20020012963A1
GENERAL INFORMATION:

APPLICANT: Morgensztejn, Jay P.
APPLICANT: Kanieczny, Andrzej
APPLICANT: Bazindauskas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIV & COCKFIELD, LLP
STREET: 28 State Street

us-09-944-326-4.11m.rnpb

Search completed: November 8, 2003, 04:48:00
Job time : 241 secs

? APPLICATION NUMBER: PCT/US93/12468
 ? FILING DATE: 1993-DEC-30
 ? APPLICATION NUMBER: US 08/156,549
 ? FILING DATE: 1993-NOV-22
 ? APPLICATION NUMBER: US 07/999,712
 ? FILING DATE: 1992-DEC-31
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: DIGIORGIO, Jeanne M.
 ? REGISTRATION NUMBER: 41,710
 ? REFERENCE/DOCKET NUMBER: IMI-026C2CNCBPADV
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (617) 227-7400
 ? TELEFAX: (617) 742-4214
 ? INFORMATION FOR SEQ ID NO: 35:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 31 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: cDNA
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 ? US-10-196-107A-35
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 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 24 AGGAGCAGGGCTTTCATC 7

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

4 nucleic - nucleic search, using sw model

on on: November 8, 2003, 00:42:33 ; Search time 2054 Seconds

(without alignments)
248.488 Million cell updates/sec

File: US-09-944-326-4

Sequence: 1 cagcagcagagctcctcatcat 21

Sorting table: IDENTITY NUC

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Marched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_earth:
3: em_earth:
4: em_earth:
5: em_earth:
6: em_earth:
7: em_earth:
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9: gb_earth:
10: gb_earth:
11: gb_earth:
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13: gb_earth:
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29: gb_earth:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	100	10	BP920141
3	21	100.0	102	10	BP958934
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C	5	21	100.0	124	12	BM821731	BM821731 K-EST0090
C	7	21	100.0	138	13	BQ339862	BQ339862 PM1-NN120
C	8	21	100.0	142	14	D45267	D45267 HUMG1194 H
C	9	21	100.0	147	13	BQ339466	BQ339466 PM1-NN120
C	10	21	100.0	148	10	BF846357	BF846357 PM1-EN006
C	11	21	100.0	149	14	R47195	R47195 CBS-389 Sub
C	12	21	100.0	169	10	BE766895	BE766895 RC2-NT011
C	13	21	100.0	177	9	AL048592	AL048592 DKF25868
C	14	21	100.0	183	12	BI032792	BI032792 MR4-NN018
C	15	21	100.0	184	10	BP958930	BP958930 PM1-NN120
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C	17	21	100.0	196	9	AT745406	AT745406 wcl341.x
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C	24	21	100.0	236	10	BP948789	BP948789 MR3-NN021
C	25	21	100.0	238	10	BF923639	BF923639 MR4-NT014
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C	40	21	100.0	265	10	BP961152	BP961152 PM1-NN120
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C	42	21	100.0	269	10	BP948799	BP948799 MR3-NN021
C	43	21	100.0	269	13	BQ339911	BQ339911 MR3-NN021
C	44	21	100.0	272	10	BF956582	BF956582 PM1-NN120
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence.
AM276802
AM276802.1 GI:6663832
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 85)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco.
Location/Qualifiers

1. 85
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/db_xref="taxon:9606"
/clone="IMAGE:2745288"
/sex="female"
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/db_host="DB108"
/note="Organ: ovary; Vector: PAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the UNG sites of PAMP10. Size selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA library preparation: David B. Kitzman, Ph.D (NCI). Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."

18 COUNT 18 a 21 c 30 g 16 t
Query Match 100.0%; Score 21; DB 9; Length 85;
Best Local Similarity 100.0%; Pred. No. 29;
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1 CAGCAGCAGGCTTCATCAT 21
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BP920141 100 bp mRNA linear EST 19-JAN-2001
PM1-NN1200-071100-003-f02 NT0179 Homo sapiens cDNA, mRNA sequence.
BP920141 GI:12316029
EST.
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
PUBMED
MENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM1&f2=PM1-NT0179-071100-003-f02&f3=2000-11-07&f4=1)
Seq primer: puc 18 forward
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Location/Qualifiers

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/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 21 a 34 c 20 g 25 t
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Best Local Similarity 100.0%; Pred. No. 31;
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1 CAGCAGCAGGCTTCATCAT 21
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PM1-NN1200-011200-009-b07 NN1200 Homo sapiens cDNA, mRNA sequence.
BP958934
BP958934 GI:12376209
EST.
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM1&f2=PM1-NN1200-011200-009-b07&f3=2000-12-01&f4=1)
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SESSION B0339862 GI:20999978
 REGION EST.
 WORDS Homo sapiens (human)
 ORIGIN Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 138)
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-NN1200-
 011200-010-f07&c3=2000-12-01&c4=1)
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 Site 2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
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 127 CAGCAGCAGAGCTTCATCAT 107

TITLE High-density cDNA filter analysis of the expression profiles of the
 gene preferentially expressed in human brain
 JOURNAL Gene 164, 219-227 (1995)
 MEDLINE 96069586
 PUBMED 7590334
 COMMENT Contact: Nobuaki Takahashi
 Institute of Medical Science
 University of Tokyo
 Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108
 Tel: 03-5449-5625
 Fax: 03-5449-5445.
 FEATURES
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 DEFINITION PM1-NN1200-051100-004-h12 NN1200 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B0339466
 VERSION B0339466.1 GI:20999152
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 147)
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-NN1200-
 051100-004-h12&c3=2000-11-05&c4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 34.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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/dev stage="Adult"
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Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
RSG COUNT 35 a 46 c 28 g 38 t
RIGIN

Query Match 100.0%; Score 21; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAGCAGCAGAGCTTCATCAT 21
122 CAGCAGCAGAGCTTCATCAT 142

RESULT 9
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XUS BF846357 PM1-EN0065-231000-002-b01 EN0065 Homo sapiens CDNA, mRNA sequence.
XUS BF846357.1 GI:12233611
XUS EST.
XUS Homo sapiens (human)
XUS Homo sapiens
XUS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 148)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bionnes, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED 2020263
10737800
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Ludwig Institute for Cancer Research
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&cl2=PM1-EN0065-
231000-002-b01&cl3=2000-10-23&cl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 110.
Location/Qualifiers
1. 148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev stage="Adult"
/clone_lib="EN0065"
/note="Organ: lung, normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ATTUES
source
38 COUNT 24 a 56 c 41 g 27 t

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAGCAGCAGAGCTTCATCAT 21
34 CAGCAGCAGAGCTTCATCAT 54

RESULT 10
R47195/c 149 bp mRNA linear EST 12-DEC-1995
LOCUS
DEFINITION
CBS-389 Subtractive cDNA library, ocular ciliary body Homo sapiens
CDNA clone CBS-389 5' end similar to TRPM-2 (clusterin) (accession
number M64722), mRNA sequence.
R47195
R47195.1 GI:807537
EST.
XUS Homo sapiens (human)
XUS Homo sapiens
XUS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 149)
Escarbano, J., Ortega, J. and Coca-Prados, M.
Isolation and characterization of cell-specific cDNA clones from a
subtractive library of the ocular ciliary body of a single normal
human donor: Transcription and synthesis of plasma proteins
J. Biochem. 118 (5), 921-931 (1995)
96318503
8749308

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Coca-Prados, M.
Department of Ophthalmology and Visual Science
Yale University Medical School
330 Cedar Street, New Haven, CT 06520-8061
Tel: 2037852742
Fax: 2037856123
Email: miguel.coca-prados@quickmail.yale.edu
Seq primer: T3.
Location/Qualifiers
1. 149
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="CBS-389"
/note="Vector: Bluescript II SK, Site 1: EcoRI, Site 2:
hybridizing antisense, single-stranded phagemid DNA (ssDNA
) (as phibscript SK-) from the ocular ciliary body CDNA
library (target) of a 34-year-old female donor in
lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular
cell line cDNA library (driver) in the same vector."

FEATURES
source
1. 149
Location/Qualifiers
1. 148
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="CBS-389"
/note="Vector: Bluescript II SK, Site 1: EcoRI, Site 2:
hybridizing antisense, single-stranded phagemid DNA (ssDNA
) (as phibscript SK-) from the ocular ciliary body CDNA
library (target) of a 34-year-old female donor in
lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular
cell line cDNA library (driver) in the same vector."
BASE COUNT 33 a 31 c 56 g 29 t
ORIGIN

Query Match 100.0%; Score 21; DB 14; Length 149;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAGCAGCAGAGCTTCATCAT 21
71 CAGCAGCAGAGCTTCATCAT 51

RESULT 11
BE766895/c 169 bp mRNA linear EST 19-SEP-2000
LOCUS
DEFINITION
RC2-NT0110-050600-013-f03 NT0110 Homo sapiens CDNA, mRNA sequence.
ACCESSION
BE766895
BE766895.1 GI:10196819
KEYWORDS
EST.

ORIGIN Homo sapiens (human)
ORIGIN Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=4&2=RC2-WT0110-050>)
 600-013-f036c3-2000-06-05&4=1)
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 High quality sequence start: 18
 High quality sequence stop: 169.
FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="WT0110"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from OESTRES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 37 a 36 c 59 g 37 t
ORIGIN
 Query Match 100.0%; Score 21; DB 10; Length 169;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CAGCAGCAGGCTTCATCAT 21
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 59 CAGCAGCAGGCTTCATCAT 39
TITLE AL048592 177 bp mRNA linear EST 01-MAR-2000
JOURNAL DKFZ586H092_r1 586 (synonym: hute1) Homo sapiens cDNA clone
HEADLINE 20202663
PUBLISHED 10737800
COMMENT Contact: Simpson, A.J.G.
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 Ludwig Institute for Cancer Research
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 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
ORIGIN Homo sapiens (human)
ORIGIN Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

COMMENT Contact: Pousetka A.J.
 Department Lehrach
 Max-Planck-Institute for Molecular Genetics
 Ihnestrasse 73, 14195 Berlin, Germany
 Tel: +49-30-84131623
 Fax: +49-30-84131128
 Email: pousetka@mpimg-berlin-dahlem.mpg.de
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 31 sequence available.
 This clone (DKFZ586H092) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
 Location/Qualifiers
 1. 177
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="DKFZ586H092"
 /tissue_type="uterus"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="586 (synonym: hute1)"
 /note="Vector: pSPoriT, Site 1: NotI; Site 2: SalI/MluI"
BASE COUNT 40 a 41 c 64 g 32 t
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 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CAGCAGCAGGCTTCATCAT 21
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 77 CAGCAGCAGGCTTCATCAT 57
RESULT 13
 B1032792 183 bp mRNA linear EST 14-JUN-2001
LOCUS B1032792
DEFINITION MR4-NN0188-220101-204-e01 NN0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION B1032792
VERSION B1032792.1 GI:14439418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORIGIN Homo sapiens
ORIGIN Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

BE COUNT 41 a 42 c 62 g 40 t
GIN

Query Match 100.0%; Score 21; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGCAGCAGAGTCTTCATCAT 21
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43 CAGCAGCAGAGTCTTCATCAT 23

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Time : 2057 secs